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AAB61139
AAU86151
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AAM43652
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ALIGNMENTS

Human SIGIRR protein

08-SEP-1999 AAY25426;

(first entry)

AAY25426 standard; Protein; 410

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RESULT 1
AAY25426
ID AAY25427
XX AAY25426
AC AAX2
XX Huma
XX SIGI
KW SIGI
KW Lintek
KW Lintek
KW Lintek
KW Lintek
KW Lintek
KW Oblac
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     WPI; 1999-418925/35
N-PSDB; AAX88091.
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Claim

2; Page 69-71; 72pp; English

New interleukin-1 receptor analog SIGIRR nucleic acid

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proteins

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RESULT 2
AAB61139
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CC description of the SIGIRR gene. The proteins of the invention are used:

CC description of the signal transduction and inflammation; (ii) to cidentify and purify proteins that associate with SIGIRR grands and for, and rational design of, potential inhibitors of activity; (iv) congenita, 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local :
     03-JUN-1999;
16-MAR-2000;
22-MAR-2000;
                                                                                                                                                                                                                                                                                  Human; NOVX; antiinflammatory; cytostatic; neuroprotective; cerebroprotective; immunomodulator; vulnerary; vasotropic; gene therapy; hyperplasia; tumour; restenosis; psoriasis; Dupuytren's contracture; diabetes; rheumatoid arthritis; cerebral oedema; Alzheimer's disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB61139 standard;
                                                                                              01-JUN-2000;
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                                                                                                                                              14-DEC-2000
                                                                                                                                                                                         WO200075321-A2
                                                                                                                                                                                                                                       Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPGVCDRAPDFLSPSEDQVLRPALGSSVALNCTAWVVSGPHCSLPSVQWLKDGLPLGIGG
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Similarity 100.0%;
18; Conservative (
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99US-0137322.
2000US-0189810.
2000US-0191158.
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                                                                                                2000WO-US15303
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Pred. No. 1.6e-57;
Mismatches 0;
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11-FEB-2000; 2000WO-US03565

99WO-US05028

WO200153486-A1.

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ANU86115
ID A2
XX A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PRO342 polypeptide.
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31-MAY-2000; 2000US-0137322
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Pred. No. 1.6e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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RESULT 4
AAU17408
ID AAU1
XX
AC AAU1
XX
DT 07-1
XX
Neu
KW Neu
KW 1mm
KW orgg
KW sicl
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atches
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11 MAY 1999
02 JUN-1999
22 JUN-1999
22 JUN-1999
20 JUL-1999
26 JUL-1999
28 JUL-1999
17 AUG-1999
31 AUG-1999
01 SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists or anti-PRO antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. AAU86128-AAU86162 represent the human PRO
            Neuroprotective: cytostatic; dermatological; immunosuppressive; tumour; antiinflammatory; anti-HIV; antibacterial; antiinflammatory; cancer; immune system disorder; rheumatoid arthritis; inflammatory condition; organ transplant rejection; infection; hepatitis C; blood disorder;
                                                                                                             07-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 61; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Thirty five nucleic acids encoding PRO polypeptides, useful for treating benign or malignant tumours, leukaemias and lymphoid malignancies, inflammatory, anglogenic and immunologic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI;
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                Novel signal
                                                                                                                                        AAU17408
                                                                                                                                                                  AAU17408 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                               polypeptides of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watanabe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Marsters
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                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                          _
                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention relates
                                                                                                                                                                                                                                                                                      MPGVCDRAPDFLSPSEDQVLRPALGSSVALNCTAMVVSGPHCSLPSVQWLKDGLPLGIGG
                                                                                                                                                                                                                                                  HYSLHEYSWVKANLSEVLVSSVLGVNVTSTEVYGAFTCSIQNISFSSFTLQRAGPTSH 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-205567/26.
DB; ABK40277.
                                                                                                                                                                                                                                    HYSLHEYSWVKANLSEVLVSSVLGVNVTSTEVYGAFTCSIQNISFSSFTLQRAGPTSH 118
                                                                                                                                                                                                                                                                                                                                                118;
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                                                                                                                                                                                                                                                                                                                                             100.
nilarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                     504
anaemia; hyperproliferative
                                                                                transduction pathway protein,
                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000WO-US0021
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48; 302pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pan J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99WO-US21090.
99WO-US28313.
99WO-US28301.
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99US-149395P.
99US-151689P.
99WO-US20111.
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99US-140653P.
99US-144758P.
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99US-133459P.
99WO-US12252.
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Pan J, Pitti RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US28634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-145698P
                                                                                                                                                                  Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                invention.
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                                                                                                                                                                  407
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Pred. No. 2e-57;
; Mismatches 0;
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 disorder; Gaucher's disease;
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Smith V,
                                                                                Seq ID
                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                         60
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  12-SEP-2000;
14-SEP-2000;
14-SEP-2000;
                                                                                                                                    22-AUG-2000;
22-AUG-2000;
23-AUG-2000;
30-AUG-2000;
01-SEP-2000;
01-SEP-2000;
01-SEP-2000;
05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
08-SEP-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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                                                                                                          08-SEP-2000
08-SEP-2000
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22-AUG-2000;
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14-AUG-2000;
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14-JUL-2000;
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07-JUN-2000;
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17-MAR-2000;
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04-FEB-2000;
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14-AUG-2000;
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2000US-0229509
2000US-0229519
2000US-0230437
2000US-02310438
2000US-0231243
2000US-0231243
2000US-0231243
2000US-0231243
2000US-0231244
2000US-0231414
          2000US-0232080.
2000US-0232081.
2000US-0231968.
2000US-023397.
2000US-0232397.
2000US-0232398.
2000US-0232399.
2000US-0232400.
2000US-0232401.
2000US-0233063.
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2000US-0224518
2000US-0225213
2000US-0225214
2000US-0225266
2000US-0225266
2000US-0225268
2000US-0225277
2000US-0225277
2000US-0225777
2000US-0225757
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2000US-0217487.
2000US-0217496.
2000US-0218290.
2000US-0220963.
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2000US-0215135.
2000US-0216647.
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2000US-0205515.
2000US-0209467.
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2000US-0190076
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17-NOV-2000
10-DEC-2000
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29-SEP-2000;
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29-SEP-2000;
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21-SEP-2000;
21-SEP-2000;
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2000US-0246610
2000US-0246611
2000US-0246613
2000US-0249207
2000US-0249208
2000US-0249211
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2000US-0249218
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2000US-0249218
2000US-0249218
2000US-0249292
2000US-0249292
2000US-0259198
2000US-0259198
2000US-0251869
2000US-0251869
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2000US-0246475
2000US-0246476
2000US-0246477
2000US-0246477
2000US-0246528
2000US-0246528
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2000US-0235834
2000US-0235836
2000US-0236367
2000US-0236369
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2000US-0236370
2000US-0237039
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2000US-0234223.
2000US-0234274.
2000US-0234997.
2000US-0234998.
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2000US-02
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The invention relates to novel isolated polypeptides (I), and completed polynucleotides (II). (II) and the antibody to (I) are useful for claiming the invention of the antibody to (I) are useful for conjunctions (e.g. conjenital and acquired immunodeficiencies, autoimmune conditions) organ conjunctions and graft versus host disease, infectious diseases (e.g. rheumatoid arthritis), inflammatory conditions, organ conjunctions and graft versus host disease, infectious diseases (c.g. hepatitis C), bleeding disorders, haemoglobin abnormalities and cother blood-related disorders (sickle cell anaemia), myeloproliferative conditions (e.g. Gaucher's disease and cancer), neurodegenerative condisorders (e.g. Gaucher's disease and cancer), neurodegenerative condisorders (e.g. diseamer's disease and cancer), neurodegenerative conformalities (nown syndrome), ischaemic injury (e.g. stroke), renal conformalities (nown syndrome), includers, dermatological disorders, in conformalitie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     08-DEC-2000;
08-DEC-2000;
11-DEC-2000;
05-JAN-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel polypeptides useful for diagnosing, treating, preventing and/or prognosing disorders related to the proteins, including cancers, immune disorders and neuronal disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rosen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME SCI INC
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)B; AAS27325.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; 2000US-0251989.
; 2000US-0251990.
; 2000US-0254097.
; 2001US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ID No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    973; 880pp;
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밁
           Ωy
                                Query Match
Best Local
                          Matches
l Similarity
49; Conserv
                          Conservative
                               38.3%;
                         0;
                             Score 240; DB 22;
Pred. No. 7.5e-17;
                          Mismatches
                          0;
                         Indels
                         0
                         Gaps
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Length 407;

0

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AAM43652
standard; Protein; 407
A.
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22-OCT-2001 (first entry)

AAM43652;

Human polypeptide SEQ ID NO 330.

Human; antiarthritic; antirheumatic; antiproliferative; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide, ophthalmological; cytostatic; immunosuppressive; nootropic; neuroprotective; antiallergic; hepatotropic; antidiabetic; antihifiammatory; antiulcer; vulnerary; anticonvulsant; antibacterial; antiparastic; cardiant; gene therapy; cancer; immune disorder; cardiovascular disorder; neurological disease; infection; human.

WO200155308-A2

SEP-2000; SEP-2000; SEP-2000;	26-SEP-2000; 27-SEP-2000;	SEP-2000;	SEP-2000;	SEP-2000;	14-SEP-2000;	14-SEP-2000;	14-SEP-2000;	14-SEP-2000;	14-SEP-2000;	12-888-2000;	08-SEP-2000;	-SEP-2000;	08-SEP-2000;	-SEP-2000;	08-SEP-2000;	-SEP-2000;	-SEP-2000;	05-SEP-2000;	01-SEP-2000;	01-SEP-2000;	01-SEP-2000;	23-AUG-2000;	22-AUG-2000;	22-AUG-2000; 22-AUG-2000;	18-AUG-2000;	14-AUG-2000;	14-AUG-2000;	14-AUG-2000;	14 - AUG - 2000;	14-AUG-2000;	14 - AUG - 2000;	14-AUG-2000;	14-AUG-2000;	26-JUL-2000;	26-JUL-2000;	11-JUL-2000;	11-JUL-2000;	07-JUL-2000; 07-JUL-2000;	30-JUN-2000;	28-JUN-2000;	19-MAY-2000;	18-APR-2000;	16-MAR-2000;	02-MAR-2000;	04-FEB-2000;	31-JAN-2000;	17-JAN-2001;	AUG	
2000US-0235836. 2000US-0236327. 2000US-0236367.	2000US-0235484. 2000US-0235834.	2000US-0234997. 2000US-0234998.	2000US-0234274.	2000US-0233065.	2000US-0233063.	2000US-0232401.	200008-0232399.	2000US-0232398.	2000US-0232397.	200005-0232081.	2000US-0232080.	2000US-0231414.	2000US-0231244.	2000US-0231243.	2000US-0230438.	2000US-0230437.	2000US-0229513.	2000US-0229345.	2000US-0229344.	2000US-0229343.	2000US-0228924. 2000US-0229287.	2000US-0227009.	2000US-0227182.	2000US-0226868.	2000US-0226279.	2000US-0225759.	2000US-0225757.	2000US-0225447.	2000US-0225268.	2000US-0225267.	2000US-0225266.	2000US-0225213.	2000US-0224519.	2000US-0220964.	2000US-0220963.	2000US-0217496.	2000US-0217487.	2000US-0216647. 2000US-0216880.	2000US-0215135.	2000US-0209467.	2000US-0205515.	2000US-0198123.	2000US-0189874.	2000US-0186350.	2000US-0180628.	2000US-0179065.	2001WO-US01309.		
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Barash SC, Ruben 488781/53.	N GENOME SCI INC	2001US-0259678	2000US-0251990 2000US-0254097	2000US-0251989	200005-0251868	2000US-0251856	2000US-0256719	2000US-0251988	2000US-0251030	2000US-0250160	2000US-0249300	2000US-0249297	2000US-0249265	2000US-0249264	2000US-0249244	2000US-0249218	2000US-0249217	200008-0249215	2000US-0249214	2000US-0249213	200008-0249211	200005-0249210	2000US-0249209	2000US-0249207	2000US-0246613	200005-0246611	2000US-0246609	2000US-0246532	2000US-0246527	2000US-0246526	2000US-0246525	2000US-0246523	2000US-0246478	2000US-0246476	2000US-0246475	2000US-0244617	2000US-0241826	2000US-0241808	2000US-0241787	2000US-0241785	2000US-0241221	2000US-0239937	2000US-0239935	2000US-0237040	2000US-0237038	2000US-0237037	2000US-0236370.	2000US-0236369	
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AAM43583
ID AAM4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to human polynucleotides (AAI63803-AAI64012) and CC or amediorating medical conditions e.g. by protein or gene thorapy. The CC genes were isolated from a range of human tissues disclosed in the CC specification. The nucleic acids, proteins, antibodies and (ant)agonists of the protein or gene thorapy. The CC are useful in the diagnosis, treatment and prevention of: (a) cancer, bone marrow, breast, gastrointestinal tract, liver, lung, or CC uncogenital, (b) immune disorders e.g. Addison's disease, allergies, CC conh's disease, multiple sclerosis, rheumatoid arthritis and ulcerative (c) wound healing; (e) neurological diseases e.g. cerebral anoxia and and parasitic infections diseases such as myocardial schaemias; and parasitic infections diseases such as viral, bacterial, fungal and parasitic infections diseases such as viral bacterial, fungal whose the sequence data for this patent did not form part of the CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                 31-JAN-2000;
04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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Best Local
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                                                                                                                                                                                             17-JAN-2001;
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                                                                                                                                                                                                                                                                                      Homo
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Similarity 100.0%;
19; Conservative
                            2000US-0179065.
2000US-0180628.
2000US-0184664.
2000US-0186350.
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0; Mismatches
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11-JUL-2000; 2000US-022963.
26-JUL-2000; 2000US-022526.
14-AUG-2000; 2000US-0225214.
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14-AUG-2000; 2000US-022527.
14-AUG-2000; 2000US-022575.
14-AUG-2000; 2000US-022576.
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14-AUG-2000; 2000US-022934.
20-SEP-2000; 2000US-022934.
20-SEP-2000; 2000US-02393.
20-SEP-2000; 2000US-023124.
20-SEP-2000; 2000US-023141.
20-SEP-2000; 2000US-02314.
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08-NOV-2000;
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08-NOV-2000;
     the encoded proteins (AAM434497-AAM43660) useful for preventing, treating or ameliorating medical conditions e.g. by protein or gene therapy. The genes were isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant)agonists are useful in the diagnosis, treatment and prevention of: (a) cancer,
                                                                          Claim 11;
                                                                                           treating
                                                                                                     New
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                                                      invention relates to human
                                                                                           isolated nucleic ating and/or preventing
breast and ovarian
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                                                                                                                                                  CA,
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cancer
                                                                        664pp + Sequence Listing; English.
                                                                                           and polypeptides, human diseases an
and
                                                      polynucleotides (AAI63803-AAI64012) and
other
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                                                                                           useful for diagnosing, d disorders -
of the adrenal
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treating

numerous

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RESULT 7
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Best Local :
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                                    associated proteins represented in AAB58106 - AAB58548. Lung cancer associated proteins and polynucleotide sequences, their agonists, and antagonists may have neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular active general; vulnerary; gastrointestina general; nephrotropic; antiinfective; gynecological; or antibacterial activity. The invention also includes antibodies specific for the
                                                                                                                                                                                 such
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cardioactive; immunomodulatory; muscular active; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynecological; antibacterial; diagnosis; neural disorder; immune disorder; r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and parasitic infections.

Note: The sequence data for this patent did not form printed specification, but was obtained in electronic from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 urogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative
protein or polynucleotide sequences. The lung cancer associated polynucleotide sequences may be used for detection of lung cance chromosome identification, as chromosome markers, and for numer
                                                                                                                            Polynucleotide
                                                                                                                                                        Claim
                                                                                                                                                                                             Lung cancer associated gene sequences, refeantigens, useful for treatment, prevention,
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                                                                                                                                                                                                                                                                                  Ruben
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proliferative
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                                                                                                                                                                                                                                                                                                           (HUMA-) HUMAN GENOME SCI INC (ROSE/) ROSEN C A.
                                                                                                                                                                                                                                                                                                                                                       12-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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DB; AAF18292.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer associated polypeptide sequence SEQ
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                                                                                                                                                                                lung
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healing; (e) neurological diseases e.g. cerebral anoxia an
and (f) infectious diseases such as viral, bacterial, fung
                                                                                                                                                     Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer associated
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                                                                                                                                                                                   cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disorder;
                                                                                            sequences AAF17982 - AAF18424 encode human lung carteins represented in AAB58106 - AAB58548. Lung cance teins and polynucleotide sequences, their agonists,
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diagnosis o
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disease.
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                                                                  gastrointestinal
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             lung cancer
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of disorders
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The present sequence represents a splice variant of human in signal transduction polypeptide. The polypeptide is designated H19G5. The activity. The H19G5 transcript is expressed in the heart. H19G5 earlypeptides and polynucleotides are useful for preventing or treating a cardiamyopathy, hypertrophic cardiamyopathy, restrictive cardiamyopathy, hypertrophic cardiamyopathy, restrictive cardiamyopathy, and really a cardiamyopathy, hypertrophic cardiamyopathy, restrictive cardiamyopathy, are useful or preventing a cardiamyopathy, hypertrophic cardiamyopathy, restrictive cardiamyopathy, and really a sease, aortic valve disease or tricuspid valve disease, arterial or rhenovascular hypertension, cardiac arrhythmia, pulmonary, and cardiac tumours in humans. The polypeptide is also useful for transduction or the expression of a protein capable of regulating signal or acceptor molecule of a phosphate group. The monoclonal antibodies can
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Best Local
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                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                  Novel h19G5 polypeptides capable of regulating signal transduction and exhibiting kinase activity useful for identifying antibodies to treat cardiac diseases, and additional mediators of signal transduction
                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-007013/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal transduction; H19G5; kinase; cardiac disease; angina pectoris; congestive heart failure; dilated congestive cardiomyopathy; hypertrophic cardiomyopathy; restrictive cardiomyopathy; hypertension; mitral valve disease; aortic valve disease; tricuspid valve disease; myocardial infarction; cardiac arrhythmia; arteriosclerosis; atherosclerosis; cardiac tumour; microbial infection; splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A splice variant of a signal transduction polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB30570 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     diagnostic or research purposes. The proteins may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders. The proteins may also be used in the treatment of wounds and infectious diseases. Polynucleotide sequences AAF18433 and identification and characterisation of the polynucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Page 74-76;
                                                                                                                                                                                                                                                                                                                                                                                                                                   SCIOS INC.
                                                                                                                                                                                                                                                                                                                                                                                                 Stanton L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             363 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0129553
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                                                                                                                                                                                                                                                            81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                 Kong
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 234; DB 21;
Pred. No. 2.8e-16;
0; Mismatches 1;
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RESULT 9
AAE16274
ID AAE1
                                       Yue H, Lal r, Gandhi AR, Tribouley (Gandhi AR, Tribouley (Ramkumar J, Griffin J Baughn MR, He A, The Lo TP, Khan F, Recif Cother M, Elliott V
                                                                                                                                                                                                                                           15-Jun-2000; 2000US-212073P.
23-JUN-2000; 2000US-213467P.
30-JUN-2000; 2000US-215651P.
07-JUL-2000; 2000US-216055P.
13-JUL-2000; 2000US-218372P.
25-AUG-2000; 2000US-228056P.
WPI; 20
N-PSDB;
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Best Local
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                                                                                                                                                                                                         (INCY-) INCYTE GENOMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; kinase; PKIN-20; cancer; leukaemia; adenocarcinoma; osteoporosis; immune disorder; atherosclerosis; Crohn's disease; Hodgkin's disease; Acquired Immune Deficiency Syndrome; ALDS; Addison's disease; anaemia; allergy; asthma; adult respiratory distress syndrome; multiple sclerosis; autoimmune thyroiditis; bronchitis; diabetes mellitus; osteoarthritis; rheumatoid arthritis; ulcerative colitis; cirrhosis; Costing's syndrome; fraves' disease; pancreatitis; psoriasis; rheumatoid arthritis; ulcerative colitis; cirrhosis; Cushing's syndrome; hepatitis; hypothyroidism; cerebral palsy; catarract; angina pectoris; coardiovascular disease; hypotherision; vasculitis; myocarditis; obesity; congestive heart failure; ischaemic heart disease; lung tumour; gout; fatty liver; Niemann-pick's disease; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200196547-A2
                                                                                                                                                                                                                                                                                                                                                                                                       14-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human kinase PKIN-20 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAE16274 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE16274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be used as probes for detecting discrete antigens expressed by tissue cell samples, and therefore used in humans for localization and monitoring of microbial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 LHEYSWYKANLSEVLVSS-----VLGVNVTSTEVYGAFTCSIQN 102
2002-090207/12
DB; AAD26467.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ESSSRVLISATLKNFQLLTILVVVAEDLGVYTCSVSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33;
                                 P, Bandman O, Borowsky ML, Au-Young J, Lu Y;
Tribouley CM, Walia NK, Yao MG, Lu DAM, Greenwald Sf
Griffin JA, Kearney L, Burford N, Nguyen DB, Tang Y
He A, Thornton M, Hafalia A, Patterson C, Gururajan
IN F, Recipon SA, Azimzai Y, Policky JL, Ding L;
Elliott VS, Thangavelu K, Batra S, Ison CH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                  2001WO-US19444.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       871 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
575. 827
/note= "Eukaryotic protein kinase domain"
580. 812
/label- Protein_kinase_domain
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Pred. No. 0.034;
1; Mismatches
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                                                                      AM, Greenwald SR;
DB, Tang YT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 33
                                                                                                                                                                                                                                                         hypertrophic cardiomyopathy; restrictive cardiomyopathy; hypertension; mitral valve disease; aortic valve disease; tricuspid valve disease; myocardial infarction; cardiac arrhythmia; arteriosclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Acquired Immune Deficiency Syndrome (AIDS), asthma, Addison's disease, atherosclerosis, anaemia, allergies, adult respiratory distress syndrome, autoimmune thyroiditis, gout, bronchitis, Crohn's disease, diabetes mellitus, multiple sclerosis, Good pasture's syndrome, Graves' disease, osteoarthritis, osteoporosis, pancreatitis, psoriasis, Reiter's syndrome, rheumatoid arthritis, Sjogren's syndrome, uveitis, ulcerative colitis, bacterial, parasitic, fungal, viral, protozoal and helminthic infections) growth and development disorders (arteriosclerosis, cirrhosis, hepatitis, Cushing's syndrome, hypothyroidism, cerebral palsy, cataracts); cardio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       treating a disease or condition associated with decreased expression of PKIN and a composition comprising PKIN antagonist is useful for treating a disease or condition associated with overexpression of PKIN. The disorders include cancer (leukaemia, adenocarcinoma, lymphoma, melanoma, myeloma, sarcoma, terratocarcinoma, Hodgkin's disease); immune disorder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to human kinase PKIN proteins and their corresponding cDNAs. A composition containing PKIN agonist is useful for corresponding cDNAs. A composition containing the proteins and their corresponding cDNAs. A composition containing the proteins and their corresponding cDNAs.
                                                                                                                                                                                            Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         disorder (fatty liver, Fabry's disease, Niemann-Pick's disease, hypocholesterolaemia, obesity). PKIN DNA is useful for assessing toxicity of a test compound and in gene therapy. The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vascular disease (arteriovenous fistula, hypertension, vasculitis, aneurysms, congestive heart failure, angina pectoris, myocarditis, ischaemic heart disease, chronic bronchitis, lung tumours); lipid
                    16-APR-1999;
                                                                                                                                                                                                                                       atherosclerosis;
                                                                                                                                                                                                                                                                                                                      Signal transduction; H19G5; kinase; cardiac disease; angina pectoris; congestive heart failure; dilated congestive cardiomyopathy;
                                                                                                                                                                                                                                                                                                                                                                                        Amino acid sequence of a human signal transduction polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB30567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       toxicity of a test compound is human PKIN-20 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 164-165; 197pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptides, useful for diagnosing, treating or preventing disorders of growth and development, cardiovascular and lipid, and
                                                             11-APR-2000; 2000WO-US09488
                                                                                                                                                 WO200063381-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                   19-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB30567 standard; Protein; 1351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 diseases such as cancer, comprise human kinase polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRAPTFLRELSDETV - - VLGQSVTLACQV - - - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----ESSSRVLISATLKNFQLLTILVVVAEDLGVYTCSVSN 443
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33; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                    99US-0129553
                                                                                                                                                                                                                                       cardiac tumour; microbial infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 105; DB 2
Pred. No. 0.034;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents a human protein with putative function in signal transduction. The polypeptide is designated H1965. The protein is capable of regulating signal transduction and exhibits kinase activity. The H1965 transcript is expressed in the heart. H1965 polypeptides and polynucleotides are useful for preventing or treating a cardiac disease, such as congestive heart failure, dilated congestive cardiomyopathy, hypertrophic cardiomyopathy, restrictive cardiomyopathy, mitral valve disease, aortic valve disease or tricuspid valve disease, angina pectoris, myocardial infarction, cardiac arrhythmia, pulmonary, arterial or rhenovascular hypertension, arteriosclerosis, atherosclerosis and cardiac tumours in humans. The polypeptide is also useful for detecting the expression of a protein capable of acting as a donor or acceptor molecule of a phosphate group. The monoclonal antibodies can be used as grobes for detecting a far action a far recomposition or the expression of a protein capable of acting as a donor or acceptor molecule of a phosphate group. The monoclonal antibodies can be used as grobes for detecting a far action as a consequence of a phosphate group.
                                                                                                                                                                                                                            hypertrophic cardiomyopathy; restrictive cardiomyopathy; hypertension; mitral valve disease; aortic valve disease; tricuspid valve disease; myocardial infarction; cardiac arrhythmia; arteriosclerosis;
                                                                                                                                                                                                                                                                                 Signal transduction; H19G5; kinase; cardiac disease; angina pectoris; congestive heart failure; dilated congestive cardiomyopathy;
                                                                                                                                                                                                                                                                                                                                             A full length human signal transduction polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         be used as probes for detecting discrete antigens expressed cell samples, and therefore used in humans for localization monitoring of microbial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel h19G5 polypeptides capable of regulating signal transduction and exhibiting kinase activity useful for identifying antibodies to treat cardiac diseases, and additional mediators of signal transduction -
                                                                                                                                                                                                          atherosclerosis; cardiac
                                                                                                                                                                                                                                                                                                                                                                                  19-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                        AAB30568;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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                     16-APR-1999;
                                                       11-APR-2000; 2000WO-US09488.
                                                                                                                                  WO200063381-A1
                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB30568 standard; Protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 LHEYSWVKANLSEVLVSS------VLGVNVTSTEVYGAFTCSIQN 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6 DRAPDFLSPSEDQVLRPALGSSVALNCTAWVVSGPHCSLPSVQ--WLKDGLPLGIGGHYS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ESSSRVLISATLKNFQLLTILVVVAEDLGVYTCSVSN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stanton L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1351 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                     99US-0129553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kong
                                                                                                                                                                                                              tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Η;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 105; DB Pred. No. 0.06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SAQPAAQATWSKDGAPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 by tissue or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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PR R R PR
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AAB85504
ID AAB85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Дb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a human protein with putative function of in signal transduction. The polypeptide is designated H19G5. The protein considering and protein is capable of regulating signal transduction and exhibits kinase of activity. The H19G5 transcript is expressed in the heart. H19G5 cardionyopathy. The H19G5 transcript is expressed in the heart. H19G5 cardionyopathy and protein are useful for preventing or treating of cardionyopathy, hypertrophic cardionyopathy, restrictive cardiomyopathy, and the pectoris, myocardial infarction, cardiac arrhythmia, pulmonary are arterial or thenovascular hypertension, arteriosclerosis, atherosclerosis, and cardiac tumours in humans. The polypeptide is also useful for cardioaction or the expression of a protein capable of regulating signal conscious molecule of a phosphate group. The monoclonal antibodies can cell samples, and therefore used in humans for localization and tissue or component to the service of the constant of the protein capable of acting as a donor constant of the capable of acting as a donor constant of the capable of acting as a donor constant of the capable of acting as a donor constant of the capable of acting as a donor constant of the capable of acting as a donor constant of the capable of acting as a donor constant of the capable of acting as a donor constant of the capable of acting as a donor constant of the capable of acting as a donor constant of the capable of acting as a donor constant of the capable of acting as a donor constant of the capable of acting as a donor constant of the capable of acting as a donor constant of the capable of acting as a donor constant of the capable of acting as a donor constant of the capable of acting as a donor cap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 33; Conser
                                                                                                                                                                                                                            Protein kinase; enzyme; cytostatic; nootropic; neuroprotective; human; antiparkinsonian; virucide; antibacterial; antifungal; antimigraine; analgesic; hypotensive; hypertensive; immunosuppressive; antiallergic; antipsoriatic; antirheumatic; antiarthritic; ophthalmological; anorectic; osteopathic; thrombolytic; antiarteriosclerotic; antiasthmatic; vasotropic; antidiabetic; gene therapy.
                                                                25-JAN-2001;
                                                                                                                                                        WO200155356-A2
                                                                                                                                                                                                         Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB85504 standard;
                                                                                                                                                                                                                                                                                                                                                                                                  Human protein kinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                25-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB85504;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1146 -----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1102 DRAPTFIRELSDETV--VLGQSVTLACQV-----SAQPAAQATWSKDGAPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 61-65; 81pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel h19G5 polypeptides capable of regulating signal transduction exhibiting kinase activity useful for identifying antibodies to traceardiac diseases, and additional mediators of signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 LHEYSWVKANLSEVLVSS-----VLGVNVTSTEVYGAFTCSIQN 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (SCIO-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 DRAPDFLSPSEDQVLRPALGSSVALNCTAWVVSGPHCSLPSVQ--WLKDGLPLGIGGHYS 63
                                                                                                                                                                                                      sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2001-007013/01
DB; AAC62286.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Stanton L,
2000US-0178078
2000US-0179364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --ESSSRVLISATLKNFQLLTILVVVAEDLGVYTCSVSN 1182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1610 AA;
                                                                2001WO-US02337
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein;
                                                                                                                                                                                                                                                                                                                                                                                               SGK145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Kong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 105; DB 2
Pred. No. 0.075;
l; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1610;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1145
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RESULT 13
AAE24151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention provides human protein kinases and protein kinase-like CC enzymes and polynucleotides encoding the polypeptides. The kinase CC enzymes and their modulators are useful for treating a disease or CC disorder such as cancer, immune-related diseases, cardiovascular disease or CC brain or neuronal-associated disease and metabolic disorders, including CC central nervous system, disease of the peripheral nervous system, cancers of hematopoletic origin, diseases of the CC Allaheimer's disease, Parkinson's disease, multiple sclerosis, amyotrophic CC lateral sclerosis, viral infections, infections caused by prions, CC lateral and fungi, ocular diseases, multiple sclerosis, amyotrophic bacteria and fungi, ocular diseases, migraines, pain, sexual dysfunction, Mypertension, psychotic disorders, cognition disorders, hypotension, CC metabolic disorders, and organ transplant rejection. They are also useful osteoarthritis, autolimunity, atherosclerosis, psoriasis, CC influmnatory bowel disease, rheumatory belvic disease, chronic cinflumnatory bowel disease, rheumatory atherosclerosis, psoriasis, CC injury, coronary thrombosis, clotting disorders and atherosclerosis, CC cultar diseases such as glaucoma, retinopathy and macular degeneration, CC dementia, manic depression, etc. The polynucleotides are useful in gene CC AABB5491-85522 represent the human protein kinases of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local S
Matches 33
Human; kinase; PKIN; cancer; immune system disorder; atherosclerosis; acquired immune deficiency syndrome; AIDS; Addison's disease; allergy; asthma; multiple sclerosis; psoriasis; arteriosclerosis; cirrhosis; development; hepatitis; cardiovascular; hypertension; drug screening; myocardial infarction; Goodpasture's syndrome; lipid disorder; growth; fatty liver; Gaucher's disease; Niemann-Pick's disease; anorectic;
                                                                                                                                    Human kinase
                                                                                                                                                                                                          AAE24151;
                                                                                                                                                                                                                                        AAE24151 standard; Protein; 1665
                                                                                                                                                                                                                                                                                                                                    1154 -----
                                                                                                                                                                        23-SEP-2002
                                                                                                                                                                                                                                                                                                                                                                                                        1110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17-FEB-2000;
17-MAR-2000;
29-MAR-2000;
13-NOV-2000;
                                                                                                                                                                                                                                                                                                                                                       64 LHEYSWYKANLSEVLVSS------VLGVNVTSTEVYGAFTCSIQN 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kinase polypeptides useful for treating cancers, Alzheimer's disease, viral infections, diabetes, obesity, organ transplant rejection and rheumatoid arthritis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plowman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SUGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                  6 DRAPDELSPSEDQVLRPALGSSVALNCTAWVVSGPHCSLPSVQ---WLKDGLPLGIGGHYS
                                                                                                                                                                                                                                                                                                                                                                                               DRAPTFLRELSDETV -- VLGQSVTLACQV-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 Similarity
33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1618
                                                                                                                                                                                                                                                                                                                       -ESSSRVLISATLKNFQLLTILVVVAEDLGVYTCSVSN 1190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; 2000US-0183173.
; 2000US-0190162.
; 2000US-0193404.
; 2000US-0247013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             215; 218pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16.8%;
                                                                                                                                    protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Manning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 105; DB 22;
Pred. No. 0.075;
l; Mismatches 29;
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                                                                                                                                                                                                                                                                                                                                                                                             -SAQPAAQATWSKDGAPL---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Martinez
                                                                                                                                                                                                                                                                                                                                                                                                                                                             32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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hypercholesterolaemia; obesity;

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treating and preventing cancer, an immune system disorder (e.g., cardinary).

cardinary and preventing cancer, an immune system disorder (e.g., cardinary).

casthma, atherosclerosis, multiple sclerosis, psoriasis), disease, allergy, asthma, atherosclerosis, multiple sclerosis, psoriasis), disorders

casthma, atherosclerosis, multiple sclerosis, attentions, attenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human kinase polypeptide, for diagnosing, preventing and treating cancer, immune system disorders, growth and development disorders, cardiovascular disorders and lipid disorders .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 182-186; 210pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-NOV-2000;
09-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-OCT-2000;
27-OCT-2000;
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hyperlipidaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid sequences. PKIN and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates human kinases (PKIN) and their corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yao MG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-NOV-2000;
22-NOV-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2002-454603/48.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               an R, Baughn MR, Walia NK, Elliott VS, Xu Y, Arviz
Ramkumar J, Ding L, Tang YT, Hafalia AJA, Nguyen
ARR, Lu Y, Yue H, Burford N, Bandman O, Tribouley C
Recipon SA, Lu DAM, Borowsky ML, Thornton M, Swaz
Blu K, Khan FA, Ison CH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-245708P.
2000US-247672P.
2000US-249565P.
2000US-252730P.
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1174..1235
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167..401
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1369..1621
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hypotensive; cardiant; nephrotropic;
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Sequence

1665 AA

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Matches

Conservative

11;

Score 105; DB 2 Pred. No. 0.078; 1; Mismatches

23; 29;

Length 1665;

Indels

32;

Gaps

5;

63

Query Match Best Local Similarity

16.8%;

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1157 DRAPTFLRELSDETV--VLGQSVTLACQV-----SAQPAAQATWSKDGAPL-----

DRAPDFLSPSEDQVLRPALGSSVALNCTAWVVSGPHCSLPSVQ--WLKDGLPLGIGGHYS

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RESULT 14
AAO15372
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                       The invention comprises the amino acid and coding sequences (located on chromosome I) of a human kinase protein that is related to the myosin light chain kinase subfamily. The human kinase DNA and protein sequences of the invention are useful for identifying agents that modulate the activity of the human kinase protein. Kinase-modulating agents are useful for treating a disease or condition mediated by a human kinase protein. The human kinase DNA sequences can be used to produce transgenic animals which are useful for studying the function of kinase proteins and identifying/evaluating modulators of kinase protein activity. The present amino acid sequence represents the human kinase protein of the invention.
                                                                                                                                                                                                                        New kinase proteins related to myosin light chain kinase subfamily and encoding polynucleotide, useful for diagnosing, treating disease or condition mediated by the kinase protein and for identifying modulator
                                                                                                                                                                                                                                                                                                WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; gene therapy; chromosome 1; kinase protein; myosin light chain kinase subfamily; kinase protein-mediated disease; transgenic animal.
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Sequence
                                                                                                                                                                                 Claim 1; Fig
                                                                                                                                                                                                                                                                                                                         Wei M,
                                                                                                                                                                                                                                                                                                                                                                                14-NOV-2000;
17-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human myosin light chain kinase subfamily-related kinase protein.
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DB; AAL43908, A
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1665
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2001US-0858664
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AA;
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                                                                                                                                                                                 96pp; English.
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31.4%;
                                                                                                                                                                                                                                                                                                                          Francesco
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                                                                                                                                                                                                                                                                                                                         Beasley
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                                                                                                                                                                                                                          modulators
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The present sequence represents a splice variant of human in signal CC transduction polypeptide. The polypeptide is designated H1965. The CC protein is capable of regulating signal transduction and exhibits kinase CC activity. The H1965 transcript is expressed in the heart. H1965 CC polypeptides and polynucleotides are useful for preventing or treating a CC cardiac disease, such as congestive heart failure, dilated congestive CC cardiomyopathy, hypertrophic cardiomyopathy, restrictive cardiomyopathy, hypertrophic cardiomyopathy, restrictive cardiomyopathy, cardiac arrhythmia, pulmonary, CC angina pectoris, myocardial infarction, cardiac arrhythmia, pulmonary, CC arterial or rhenovascular hypertension, arteriosclerosis, atherosclerosis and cardiac tumours in humans. The polypeptide is also useful for CC detecting the expression of a protein capable of regulating signal CC transduction or the expression of a protein capable of acting as a donor CC cell samples, and therefore used in humans for localization and CC monitoring of microbial infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel h19G5 polypeptides capable of regulating signal transduction and exhibiting kinase activity useful for identifying antibodies to treat cardiac diseases, and additional mediators of {}^\bullet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Signal transduction; H19G5; kinase; cardiac disease; angina pectoris; congestive heart failure; dilated congestive cardiomyopathy; hypertrophic cardiomyopathy; restrictive cardiomyopathy; hypertension; mitral valve disease; aortic valve disease; tricuspid valve disease; myocardial infarction; cardiac arrhythmia; arteriosclerosis; atherosclerosis; cardiac tumour; microbial infection; splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1201
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N-PSDB; AAC62287.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SCIOS INC.
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1094..1351
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Sequence

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Best Local Similarity
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                                                             2088 DRAPTFLRELSDETV--VLGQSVTLACQV-----SAQPAAQATWSKDGAPL-----
                               64 LHEYSWVKANLSEVLVSS-----VLGVNVTSTEVYGAFTCSIQN 102
                                                                                   6 DRAPDFLSPSEDQVLRPALGSSVALNCTAWVVSGPHCSLPSVQ--WLKDGLPLGIGGHYS 63
                                                                                                                              Conservative
ESSSRVLISATLKNFQLLTILVVVAEDLGVYTCSVSN 2168
                                                                                                                            16.8%; Score 105; DB 22; 31.4%; Pred. No. 0.14; :ive 11; Mismatches 29;
                                                                                                                              29;
                                                                                                                                                            Length 2596;
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                                                                                                                            32;
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Search completed: November 14, 2002, 17:30:01 Job time: 38 secs

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Result
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Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tal number of hits satisfying chosen parameters:
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81.5
81.5
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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AE350065
S50065
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fibroblast growth
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ALIGNMENTS

N;Alternate names: Cn3B protein C;Species: Gallus gallus (chicken) C;Species: Gallus gallus (chicken) C;Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 17-Mar-1999 C;Accession: PN0568 R;Maruyama, K.; Endo, T.; Kume, H.; Kawamura, Y.; Kanzawa, N.; Nakauchi, Y.; Kimura, Biochem. Biophys. Res. Commun. 194, 1288-1291, 1993 A;Title: A novel domain sequence of connectin localized at the 1 band of skeletal mus A;Reference number: PN0568; MUID:93356802; PMID:8352787 A;Accession: PN0568 A;Molecule type: mRNA A;Residues: 1-1323 <MARP A;Cross-references: DDBJ:D16541; NID:g391629; PID:d1004495; PID:g391630 A;Experimental source: skeletal muscle C;Comment: This protein string-like single molecule spans from the Z line to the M li RESULT 1 I38346 RESULT PN0568 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-7962 <RES> R:Labeit, S.; Kolmerer, B. Science 270, 293-296, 1995 Science 270, 293-296, 1995 A;Title: Titins: giant proteins in charge of muscle ultrastructure A;Reference number: A57430; MUID:96026330; PMID:7589978 A;Accession: 138346 elastic titin - human (fragme C;Species: Homo sapiens (man) C;Date: 29-May-1998 #sequence C;Accession: I38346 A;Cross-references: GDB:127867; OMIM:188840 A;Map position: 2q31-2q31 connectin 3B - chicken (fragment) C; Genetics: A;Cross-references: EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017427 A; Gene: GDB:TTN Best Query Match Matches 1937 1883 51 Local KDGLPLGIGGHYSL--HEYSWVKANLSEVLVSSVLGVNVTSTEVYGAFTCSIQNIS 104 DFGSSSCDAYLRVLDQNIPPSFTKKLTKMDKVLGSSIHMECK---VSG---SLPISAQWF 1936 KDGKEISTSAKYRLVCHERS....-VS--LEVNNLELEDTANYTCKVSNVA 1980 38; Similarity human (fragment) Conservative #sequence_revision 14.9%; Score 93.5; Pred. No. 4 Mismatches 29-May-1998 #text_change DB 32; <u>ب</u> Length 7962; Indels 39; and Gaps elasticity 7;

QΥ

Query Match

Score 91.5;

DB

2;

Length 1323;

В Qy

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A;Cross-references: EMBL:X15423; NID:g6897; PIDN:CAA33463.1; PID:g6898 A;Experimental source: var. Bristol R;Benian, G.M.; Kiff, J.E.; Neckelmann, N.; Moerman, D.G.; Waterston, I
                                                                                                                                                                                                                                                                                                                        chin [similarity] - Caenorhabditis elegans
N;Contains: protein kinase (EC 2.7.1.-)
C;Species: Caenorhabditis elegans
C;Date: 28-Oct-1995 #sequence_revision 24-Oct-1997 #text_change 20-Jun-2000
C;Accession: S57242; S0757; S06797; S57218; T27934; T28030
R;Benian, G.M.; L'Hernault, S.W.; Morris, M.E.
submitted to the EMBL Data Library, February 1993
A;Description: Additional sequence complexity within twitching of Caenorhabda;Reference number: S57242
                                                                    submitted to the EMBL Data Library, November A; Reference number: S07571
A; Accession: S07571
A; Molecule type: DNA
A; Residues: 792-6839 <BEN2>
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                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-6839 <BEN1>
A; Cross-references: EMBL:L10351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residus: 1-6831 <STO>
A;Cross_references: GB:chr_IV; PIDN:CAA98081.1; PID:93881830; GSPDB:GN00022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  itle: Genome sequence of the nematode C. elegans: a platform for investigating biological ference number: A75000; MUID:99069613; PMID:9851916

A7500: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ela.Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; anA;Accession: A88852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R:anonymous, The C. elegans Sequencing Consortium Science 282, 2012-2018, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein unc-22 [imported] - Caenorhabditis elegans
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Gene: unc-22
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Best Local 9
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Superfamily:
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Accession: A88852
                                                                                                                                                                                                            Experimental source: var.
                                                                                                                                                                                                                                                                                                      Accession: S57242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VLRPAL-----GSSVALNCTAWVVSGPHCSLPSV--QWLKDGLPLGIGGHYSLH
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1; Mismatches
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                                            hypothetical protein ZK617.1b - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000 C;Accession: T27935; T28031 R;White, S.
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                     submitted
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A:Gene: unc-22; CESP:ZK617.1a

A:Map position: 4

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A;Residues: 'MGIPCKKCKQ',19-6839 <WIZ>
A;Cross-references: EMBL:Z73899; PIDN:(
A;Experimental source: clone ZK829
C;Comment: Lack of unc-22 leads to a co
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A;Reference number: Z20442
A;Accession: T27934
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
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A;Residues: 2-99;108-194,'Q',196-206;374-468;658-753 <BEN4>
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A;Tittle: Sequence of an unusually large protein implicated A:Reference number: S06797; MUID:90044042; PMID:2812002
A;Accession: S06797
A;Status: nucleic acid sequence not shown
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A; Residues: 'MGIPGKKCKQ', 19-6839 <WIL>
A; Cross-references: EMBL: 273897; PIDN:
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A;Residues: 806-1175;1178-1998,'Y',2000-3040,'I',3042-3335,'I',3337-5693;5696-6359,'I
A;Cross-references: EMBL:X15423
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Experimental source: clone ZK617
                                                                                                                                                                                                                                                                                                                    Matches
160
                                                                                                                                                          109
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---IFSDLGDQTYLCQLEIRGPSSSDAGQYRCNIRN 192
                                                                        YSWVKANLSEVLVSSVLGVNVTSTEVYGAFTCSIQN 102
                                                                                                                                                                                                                             RAPDFLSPSEDQVLRPALGSSVALNCTAWVVSGPHCSLPSVQWLKDGLPLGIGGHYSLHE 66
                                                                                                                                                     RGPSFV--GKPRIIPKDGGALIVMECKV-----KSASTPVAKWMKDGVPLSMGGLYHA-- 159
                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                   14.48;
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                                                                                                                                                                                                                                                                                                           21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN:CAA98081.1; GSPDB:GN00022; CESP:ZK617.1a
                                                                                                                                                                                                                                                                                                                                                        Score 90;
Pred. No.
                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                constant twitching of
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                                                                                                                                                                                                                                                                                                                                                                                            ВG
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                                                                                                                                                                                                                                                                                                                                                                                        Length 6839
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to the EMBL Data Library, ce number: 220442

May 1996

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A; Molecule type: DNA
A; Residues: 1-5175 <ATI2>
A; Cross references: EMBL:247070;
A; Experimental source: clone T099
C; Genetics:
A; Gene: CESP:F15G9.4a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 6
T20992
T20992
hypothetical protein F15G9.4a - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te)
C;Accession: T20992; T24733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: clone ZK617 R;Harris, B.
  Вþ
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                                                                                                                                           A:Map position: X

A:Map position: X

A:Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184/3; A:Introns: 85/1; 2091/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/2; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 3033/2, 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4879/1; 4941/1; 5011/1; 5077,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          submitted to the EMBL Data A; Reference number: Z19355
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-7160 <WIL>
A;Cross-references: EMBL:Z73897; PIDN:CAA98065.1; G
                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data A; Reference number: Z19929 A; Accession: T24733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: T20992
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A; Residues: 1-7160 <WI2>
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ntrons: 10/3; 61/3; 135/2; 168/3; 256/2; 379/3; 405/2; 463/1; 1/1; 3141/3; 3269/1; 6473/3; 7012/3; 7097/1; 7129/3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Experimental source: clone F15G9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene: CESP: ZK617.1b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         psidues: 1-5175 <WIL>
cross-references: EMBL:247068;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              olecule type: DNA
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MPGPRSSRTVLLHAAPQFIVKPKNTT--AAIGAIVELRCSA--AGPPH---PTITWAKDG
                      MPG------VCDRAPDFLSPSEDQVLRPALGSSVALNCTAWVVSGPHCSLPSVQWLKDG
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                                                                                32;
                                                                                                  Similarity
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28.1%;
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24.0%;
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                                                                                                                                                                                                                                                                                               PIDN:CAA87344.1;
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                                                                                              Pred.
                                                                                                Score 87.5;
Pred. No. 10;
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                                                                                                                Length 5175;
                                                                             Indels
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A; Reference number: AD3252; A; Accession: AE3507

A;Status:

preliminary

R;DelVecchio, V.G.; Kapatral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Mazur, M.; Goltsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Cal Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A;Title: The genome sequence of the facultative intracellular pathoger

pathogen

O'Callaghan,

Los, T.;

Ivanov melit Let

C; Species: Brucella melitensis
C; Date: 01-Feb-2002 #sequence_0
C; Accession: AE3507

#sequence_revision

01-Feb-2002 #text_change 15-Feb-2002

(strain

amidotransferase hisH (EC 2.4.2.-) [imported] - Brucella melitensis

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R;Sulston, J.
submitted to the EMBL Data Library,
a.Reference number: Z19355
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A;Map position: X
A;Introns: 85/1; 120/1; 334/3; 370/1; 477/2; 606/3; 664/1; 935/3; 977/1; 1051/3; 1184
A;Introns: 85/1; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 303
; 2512/2; 2593/3; 2699/3; 2759/1; 2852/1; 2889/3; 2913/3; 2941/1; 2967/3; 2991/3; 303
1; 4225/1; 4361/1; 4408/1; 4456/1; 4498/1; 4647/3; 4838/1; 4902/1; 4964/1; 5034/1; 51
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A;Residues: 1-5198 <WIL>
A;Cross-references: EMBL:247068; PIDN:CAA87336.1; GSPDB:GN00028; CESP:F15G9.4b
A;Experimental source: clone F15G9
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A;Residues: 1-5198 <WI2>
A;Cross-references: EMBL:Z47070; PIDN:CAA87345.1; GSPDB:GN00028; CESP:F15G9.4b
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-5198 <VOG>
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AE3507
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                                                                                                                                                                         MPGPRSSRTVLLHAAPQFIVKPKNTT--AAIGAIVELRCSA--AGPPH---PTITWAKDG
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                                                                                                                             LPLGIGGHYSLHEYSWVKANLSEVLVSSVLGVNVTSTEVYGAFTCSIQNISFSS 107
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                                                                                                                                                                                                                                                                                        Similarity
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                                                                                    -KLIEDSKFEIAYSH-LKVTLNSTSDSGEYTCMAQNSVGSS 4646
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28.1%;
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                                                                                                                                                                                                                                                                                        Score 87.5;
Pred. No. 10;
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                                                                                                                                                                                                                                                                 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                           Length 5198;
                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mediated cell adhesion
                                                                                                                                                                                                                                                                   29;
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                                                                                                                                                                              4607
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B-CAM protein - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens
C;Accession: 13796; #sequence_revision 12-Aug-1996 #text_change 21-Jul-2000
C;Accession: 137202; #47272
R;Campbell, IG.; Foulkes, W.D.; Senger, G.; Trowsdale, J.; Garin-Chesa, P.;
Cancer Res. 54, 5761-5765, 1994
A;Title: Molecular cloning of the B-CAM cell surface glycoprotein of epitheli
A;Accession: 137202; MUID:95042297; PMID:7954395
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Resigues: 1-588 <RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-1694 <CRO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:236293; NID:g557253; PIDN:CAA85290.1; PID:g557254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sialoadhesin - mouse
C;Species: Mus musculus (house mouse)
C;Date: 07-May-1955 #sequence_revision 21-Jul-1995 #text_change 05-Nov-1999
C;Accession: 550065
R;Crocker, P.R; Mucklow, S; Bouckson, V.; McWilliam, A.; Willis, A.C.; Gordon, EMBO J. 13, 4490-4503, 1994
A;Tittle: Sialoadhesin, a macrophage sialic acid binding receptor for haemopoietic A;Accession: S50065; MUID:95009950; PMID:7925291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 21...
""+ches 37; Conservative
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C:Superfamily: amidotransferase hish; trpG homology
C:Keywords: glycosyltransferase; pentosyltransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Residues: 1-244 <KUR>
A:Cross-references: GB:/
A:Experimental source: s
C:Genetics:
A:Gene: BMEI2043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
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                                                                                                                                                                                                                                                                                                          360 SWYKNHILLEDAHASTLHLPAVTRADTGFYFCEVONAQGS----ERSSPLS 406
                                                                                                                                                                                                                                                                                                                                                                        300 DSGAYTCQATNDMGSLVSSPLSLHVFMAEVKMNPAGPVLENETVTLLCSTPKEAPQELRY
                                                                                                                                                                                                                                                                                                                                                                                                                                       246 LSSSGRNILP---GDPVTLTCR---VNSSYPAVSAVOWARDGVNLGVTGHVLRLFSAAWN 299
                                                                                                                                                                                                                                                                                                                                       68 SWVKAN-LSEVLVSSVLGVNVTSTEVYGAFTCSIQNISFSSFTLQRAGPTS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MPGV------CDRAPDFLSPSEDQVL---RPALGSSVAL------NCTAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VV-----SGPHCSLPSVQW------LKDGLPLGIGG--HYSLHEYSWVKANLS
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                                                                                                                                                                                                                                                                                                                                                                                                                -----YSLH-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13.3%; Score 83.5; DB 2; 1
21.6%; Pred. No. 6.9;
tive 17; Mismatches 42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13.3%;
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Pred. No. 0.71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 43;
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                                                                                                                epithelial
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                                                                                                                                             Rettig, W.
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Best Local
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Вþ δÃ Дb

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fibroblast growth factor receptor 4 - rat

N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Rattus norregicus (Norway rat)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 01-F
C;Accession: JC1450; pr0191
R;Horlick, RA.; Stack, S.L.; Cooke, G.M.
A;Title: Cloning, expression and tissue distribution of the gene enc
A;Reference number: JC1450; MUID:93013049; PMID:1398143
A;Accession: JC1450
A;Molecule type: mRNA
A;Cross-references: GB:M9159; NID:9204137; PIDN:AAA41157.1; PID:92(
Neuron 6, 691-704, 1991
A;Title: An extended family of protein-tyrosine kinase genes differe
A;Reference number: PT0183; MUID:91222560; PMID:2025425
A;Accession: pT0191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A/Cross-references: GDB:120155; OMIM:111200
A/Map Position: 19q12-19q13
C:Keywords: 91ycoprotein
F:1-31/Domain: signal sequence #status predicted <SIG>
F:32-628/product: Lutheran blood group glycoprotein #status experimental <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Genetics:
A;Gene: GDB:LU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: mRNA
A;Residues: 1-628 <-RES>
A;Cross-references: EMBL:X83425; NID:9603559;
A;Note: parts of this sequence, including the
c;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lutheran blood group glycoprotein precursor - human
C:Species: Homo sapiens (man)
C:Date: 09-Mar-1996 #sequence_revision 09-Mar-1996 #text_change 05-Nov-1999
C:Accession: 138000; S51663
R:Parsons, S.F.; Mallinson, G.; Holmes, C.H.; Houlihan, J.M.; Simpson, K.L.;
Proc. Natl, Acad. Sci. U.S.A. 92, 5496-5500, 1995
A:Reference number: 138000; MUID:95296337; pMID:7777537
A:Accession: 138000; MUID:95296337; pMID:7777537
A:Accession: 138000; MUID:95296337; pMID:7777537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: B-CAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   362 DPLELSEGKVLSLPLNSSAVVNCS---VHG--LPTPALRWTKDSTPLGDGPMLSLSSITF 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 VKANLSEVLVSSVLGVNVTS 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                417 -DSNGTYVCEASLPTVPVLS 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          362 DPLELSEGKVLSLPLNSSAVVNCS---VHG--LPTPALRWTKDSTPLGDGPMLSLSSTTF 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DFLSPSEDQVLRPALGSSVALNCTAWVVSGPHCSLPSVQWLKDGLPLGIGGHYSLHEYSW 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Similarity 36.2
29; Conservative
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29; Conservative
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36.2%;
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Pred. No. 3;
12; Mismatches
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Pred. No. 2.8;
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIDN:CAA58449.1; PID:g603560 amino end of the mature form,
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                                             differentially expressed
                                                                                                                   PID: g204138
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                                                                                                                                                                                                                                  encoding
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F;218-238/Domain: transmembrane #status predicted <IMM>
F;238-650/Domain: intracellular #status predicted <INT>
F;339-650/Domain: protein kinase homology <KIN>
F;313-958/Domain: protein kinase ATP-binding motif
F;321-329/Region: protein kinase ATP-binding motif
F;
RESULT 14
$18209
fibroblast growth factor receptor 4 precursor (clone fibroblast growth factor receptor 4 precursor (clone N;Alternate names: tyrosine kinase Mpk-11
N;Contains: protein-tyrosine kinase (EC 2.7.1.112)
C;Species: Mus musculus (house mouse)
C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #t
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R;Greenberg, A.S.; Steiner, L.; Kasahara, M.; Flajnik, M.F.
Proc. Natl. Acad. Sci. U.S.A. 90, 10603-10607, 1993
A;Title: Isolation of a shark immunoglobulin light chain cDNA clone encoding a protein A;Reference number: A49633; MUID:94068449; PMID:8248152
A;Accession: A49633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig lambda-like chain, V-C region - nurse shark
C;Species: Ginglymostoma cirratum (nurse shark)
C;Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       뮵
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A:Residues: 465-518 <L/
A:Experimental source:
C:Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Gene: FGF
C;Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: sequence extracted from NCBI backbone (NCBIN:141012, NCBIP:141013)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ;Superfamily: immunoglobulin V
;36-110/Domain: immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 VGSNVELLCKVYSDAQPH-----IQWLKHIVINGSSLGADGFPYVQVLKTTDINSSEV-- 161
                                                                                                                                                                                                                                                                                                                                                                                           188 YLRASDSTYSVSSLLTLSGSDWESNARFSCALTHVTLSS 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                141 LPPSPDQVQTKG-----TATLVCLANHFYPDELQVQWKKDGAVISDGVQTS----N 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69 WVKANLSEVLVSSVLGVNVTSTEVYGAFTCSIQNISFSS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12 LSPSEDQVLRPALGSSVALNCTAWVVSGPHCSLP---SVQWLKDGLPLGTGGHYSLHEYS 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 LGSSVALNCTAWVVSGPHCSLPSVQWLK----DGLPLGIGGHYSLHEYSWVKANLSEVLV 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -EVLYLRNVSAEDAGEYTCLAGNSIGLSYQS 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nmunoglobulin V region; immunoglobulin immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
#sequence_revision 07-Oct-1994 #text_change 16-Jul-1999
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29.3%;
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31.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 81;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 81.5; DB 1;
Pred. No. 3.6;
1; Mismatches 36;
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A, Note: the nucleotide sequence was submitted to the EMBL Dat R; Labelt, S.; Barlow, D.P.; Gautel, M.; Gibson, T.; Holt, J.; Nature 345, 273-276, 1990
A; Title: A regular pattern of two types of 100-residue motif A; Reference number: 146520; MUID:90238553; PMID:2129545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;462-747/Domain: protein kinase homology <KIN>
F;470-478/Region: protein kinase ATP-binding motif
F;54-98,169-221,268-330/Disulfide bonds: #status predicted
F;500,517,609/Active site: Lys, Glu, Asp #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:X57236; NID:g53187; PIDN:CAA40512.1; PID:g53188 c;Superfamily: basic fibroblast growth factor receptor 1; immunoglobulin homo C;Keywords: ATP; duplication; glycoprotein; growth factor receptor; phosphotr F;1-18/Domain: signal sequence #status predicted <SIG-F;19-99/Product: fibroblast growth factor receptor 4 #status predicted <MAT>F;19-366/Domain: extracellular #status predicted <EXT-F;19-366/Domain: immunoglobulin homology <NMN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Molecule type: mRNA
A;Residues: 1-485,'QVVRAEAFG',486-799 <STA2>
A;Cross-references: EMBL:X59927; NID:g50968; PIDN:CAA42551.1; PID:g50969
R;Gilardi-Hebenstreit, P; Nieto, M.A.; Frain, M.; Mattei, M.G.; Chestier,
Oncogene 7, 2499-2506, 1992
                                                                                                                                                                                                                                                                                  A;Title: Towards a molecular understanding A;Reference number: S20897; MUID:92258380; A;Accession: S20901
                                                                                                                                                                                                                                                                                                                                                                                R; Labeit, S.; Gautel, M.; L
EMBO J. 11, 1711-1716, 1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: An Eph-related receptor protein tyrosine kinase gene segmentally expressed A;Reference number: S30496; MUID:93096484; PMID:1281307 A;Accession: S30497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, May 1991 A; Reference number: S26751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Title: FGFR-4, a new member of the fibroblast growth factor receptor family, expres A; Reference number: $18209; MUID: $92146274; PMID: $1723680
A; Reference number: A; Accession: I46520
                                                                                                                                                                          A;Residues: 1-6805 <LAB>
A;Cross-references: EMBL:X64696
                                                                                                                                                                                                                                    A; Molecule type: mRNA
                                                                                                                                                                                                                                                                   A; Status: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: S20901; I46520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Oryctolagus cuniculus (domestic rabbit)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                titin - rabbit (fragment)
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A; Residues: 611-667 <GIL>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -QVLYLRNVSAEDAGEYTCLAGNSIGLSYQS 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSVLGVNVTSTEVYGAFTCSIQN---ISFSS 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1-799 <STA1>
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PMID:1582406
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                                                                                                                                                                                                                                                                   not shown
                                                                                                                Data Library, February 199 J.; Hsieh, C.L.; Francke,
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                                                         sequence
                                                                                                                   February 1992
L.; Francke, U
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Page 6
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.
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626
1 MPGVCDRAPDFLSPSEDQVL.....SIQNISFSSFTLQRAGPTSH
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 SwissProt_40:*
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         Gapext 0.5
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AMAL_DROME
FAS2_DROME
K6P1_CANAL
PTK7_HUMAN
PGH1_RAT
BFR2_HUMAN
CD22_HUMAN
UFO_HUMAN
PTPF_HUMAN
CTAR_HUMAN
CCC_HUMAN
                                                                                   NPHN_RAT
FGRA_HUMAN
MYEP_HUMAN
MYEP_HUMAN
NPHN_HUMAN
PGRI_HUMAN
FGRI_HUMAN
FGRI_CHICK
MITI_HUMAN
MYMI_MOUSE
DCC_MOUSE
TRIO_HUMAN
CEK2_CHICK
MYPO_HUMAN
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FGR4_MOUSE
DSCA_HUMAN
NPHN_MOUSE
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(without alignments)
376.477 Million cell updates/sec
P508995
Q031452
Q060469
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candida alb
homo sapien
trattus norv
homo sapien
                                                                   5 homo sapien
2 mus musculu
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7 mus musculu
4 rattus norv
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4 5	44	43	42	41	40	39	38	37	36	35	34
68.5	68.5	68.5	68.5	68.5	69	69	69.5	69.5	69.5	69.5	69.5
10.9	10.9	10.9	10.9	10.9	11.0	11.0	11.1	11.1	11.1	11.1	11.1
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FGR1_RAT	FGR2_XENLA	FGR3_HUMAN	FGR3_MOUSE	LDHB_FUNPA	SNI2_YEAST	MYPO_MOUSE	UFO_MOUSE	PGH1_HUMAN	VGLX_PRVRI	RAGE_RAT	XYNC_EMENI
Q04589 rat	Q03364 xer	P22607 hon	Q61851 mus	P42122 fur	P38163 sac	P27573 mus	Q00993 mus	P23219 hom	P07562 pse	Q63495 rat	
rattus norv	xenopus lae	mo sapien	s musculu	ndulus pa	ccharomyc	s musculu	s musculu	mo sapien	eudorabie	ttus norv	emericella

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SOFORMS 1 AND 2
"The DNA sequence and comparative analysis of human chromosome 20." Nature 414:865-871(2001).
cley D.R.,
Whitehead S.L., Whittaker P., Willey D.L., Williams L., Williams S
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C.M., Ross M.T., Scott C.E., Sehra H.K., Shown
B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay
Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
V.L., Martin S.L., McConnachie L.J.,
Lloyd D.M., Love
Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
Hammond S., Harrey J.L., Heath P.D., Ho S., Holden J.L., Howden E
Grafham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall F
Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
Ciegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R., Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.;
Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.
Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
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MEDLINE=21638749; PubMed=11780052;
EDON N A /TEOEOBNE 1 AND
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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Primates;
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Q9BZZZ; Q9H1H6; Q9H1H7; Q9H7L7; Q9GZS5;
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EMBL; AL109804; CAC17542.1;
EMBL; AL109804 CAC17542.1;
EMBL; AK024462; BAB15752.1;
EMBL; AK024462; BAB15749.1;
EMBL; AK024479; BAB15769.1;
EMBL; AK024479; BAB15769.1;
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MIN; 600751;
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SMART; SM00408; IGC2; I4.
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IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 5.

IG-LIKE C2-TYPE DOMAIN 6.

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IG-LIKE C2-TYPE DOMAIN 10.

IG-LIKE C2-TYPE DOMAIN 11.

IG-LIKE C2-TYPE DOMAIN 15.

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STRAIN-16M / ATCC 23456 / Biotype 1;

MEDLINE-20020109; PubMed-11756688;

DelVecchio V.G., Kapatral V., RedKar R.J., Patra G., Mujer C., Ivanova N., Anderson I., Bhattacharyya A., Lykidis A., Reznik G. Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Golts. Selkov E., Elzer P.H., Hagius S., O'Callaghan D., Letesson J.-J. Haselkorn R., Kyrpides N., Overbeek R., "The genome sequence of the facultative intracellular pathogen Brucella melitensis.";

Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
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15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last amoutation update)
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Imidazole glycerol phosphate synthase subunit hisH (EC synthase glutamine amidotransferase subunit) (IGP synthash) (Imp synthase subunit hisH) (IGP synthase subunit hisH) (IGPS subunit hisH) (IGPS subunit hisH) or BMEIZ043.
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Bacteria; Proteobacteria;
Brucellaceae; Brucella.
NCBI_TaxID=29459;
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                                                   Crocker P.R., Mucklow S., Boukson V., McWilliam A., Willis A Gordon S., Milon G., Kelm S., Bradfield P.; "Staloadhesin, a macrophage sialic acid binding receptor for haemopoletic cells with 17 immunoglobulin-like domains."; EMBO J. 13:4490-4503(1994).
                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SE STRAIN-C57BL/6; TISSUE-Macrophage; MEDLINE-95009950; PubMed-7925291;
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MEDLINE-98051930; PubMed-9383289;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MPGV------CDRAPDFLSPSEDQVL---RPALGSSVAL-----NCTAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IGP, AICAR and glutamate. The hisH subunit provides the glutamine amidotransferase activity that produces the ammonia necessary to hisF for the synthesis of IGP and AICAR (By similarity). CATALYTIC ACTIVITY: 5-[(5-phospho-1-deoxyribulos-1-ylamino)methylideneamino]-1-(5-phosphoribosyl)imidazole-4-carboxamide + L-glutamine = imidazole-glycerol phosphate + 5-aminoimidazol-4-carboxamide ribonucleotide + L-glutamate + H(2)0. PAPHWAY: Histidine biosynthesis; fifth step.

SUBUNIT: Heterodimer of hisH and hisF (By similarity). SUBCELLULAR LOCATION: Cytoplasmic (By similarity). SIMILARITY: CONTAINS 1 TYPE-1 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
                                                                                                                                                                                                                                                                                                                      (Sheep erythrocyte receptor) (SER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DVLAVTDYGGDVTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IAGDVREMVPSDASLKIPQIGWNRIHVKHSHPIFDGIPTGDDGLHAYFVHSYMLDAKNAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LPGVGAYADCRRGLDAVPGMVEALNDTVLKKARPFLGICVGMQLMSERGLEKTVTNGLGW
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196
198
216 AA;
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Pred. No. 0
                                                                                                                                                                                                                                           Sciurognathi;
                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D7156BF1985C73CF CRC64;
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                                                                                                                                                                                      SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                             Muridae;
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                                                                                                                                                                                                                      SMART; SM00410; IG_like; SMART; SM00408; IGc2; 6
                                                                                                                                                                                                                                                                                                                           MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIALIC-ACID DEPENDENT BINDING TO CELLS.
-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (ISOFORM 1) AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complex with 3' sialyllactose at 1.85 A resolution. Mol. Cell 1:719-728(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   May A.P., Robinson R.C., Vinson M., (
"Crystal structure of the N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mucklow S., Gordon S., Crocker "Characterization of the mouse Mamm. Genome 8:934-937(1997).
                                                                                                        TRANSMEM
                                                                                                                                         CHAIN
                                                                                                                                                     SIGNAL
                                                                                                                                                                                        Signal; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Purification and properties of sialoadhesin, receptor of murine tissue macrophages.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Crocker P
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                                                                                                                         DOMAIN
                                                                                                                                                                       Fransmembrane;
                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                       InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOLUBLE (ISOFORUS 2 AND 3).

SOLUBLE (ISOFORUS 2 AND 3).

ALTERNATIVE PRODUCTS: 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; AND ALTERNATIVE PRODUCED BY ALTERNATIVE SPLICING.

TISSUE SPECIFICITY: HIGHEST EXPRESSION IN SPLEEN AND LYMPH NUMBER AMOUNTS IN LUNG, LIYER, BONE MARROW, HEART AND SK EXPRESSION IN THYMUS, KIDNEY, BRAIN OR SMALL INTESTINE.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

SIMILARITY: CONTAINS 16 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.

SIMILARITY: CONTAINS 16 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: MACROPHAGE-RESTRICTED ADHESION MOLECULE STALIC-ACID DEPENDENT BINDING TO CELLS.
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U92833;

U92834;

U92837;

U92837;

U92838;

U92839;

U92839;

U92840;
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Z36233;
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Slycoprotein; Cell a
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IPR003598;
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CAA85268.1;
CAA85269.1;
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3; PubMed=2050106;
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EXTRACELLULAR (POTENTIAL)
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
IG-LIKE V-TYPE DOMAIN.
IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
                                                                                                                                         SIALOADHESIN
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1 domain of sialoadhesin
                                                                                                                                                                   Immunoglobulin domain; Repeat;
3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QF
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  SWVKAN-LSEVLVSSVLGVNVTSTEVYGAFTCSIQNISFSSFTLQRAGPTS 117
                                                                             DSGAYTCQATNDMGSLVSSPLSLHVFMAEVKMNPAGPVLENETVTLLCSTPKEAPQELRY
                                                                 LSSSGRNILP----GDPVTLTCR----VNSSYPAVSAVQWARDGVNLGVTGHVLRLFSAAWN
                                                                                                           1 Similarity 21.6
37; Conservative
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MISSING (IN ISOFORM 2).

VPPKTPTLLVFVEPOGGHQGILDCRVDSEPLAILTLHRGSQ
LVASNQLHDAPTROHIRVTAPPNALRVDIE -> CEYEPIS
ALCLSLHLTGPVQAFSSAQSKGFIGKGLRTLASSLAGCMWF
VSMLGYPALKWRILLPFWDEYRR (IN ISOFORM 3).

MISSING (IN ISOFORM 3).

MISSING (IN REF. 1; AA SEQUENCE).

P -> Q (IN REF. 1; AA SEQUENCE).

LE -> VQ (IN REF. 1; AA SEQUENCE).

T -> Q (IN REF. 1; AA SEQUENCE).

S -> Q (IN REF. 1; AA SEQUENCE).

S -> Q (IN REF. 1; AA SEQUENCE).
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01-OCT-1996 (Re
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Lutheran blood
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
Pfam; PP00047; 1g; 5.
SMART; SM00410; IG_like; 2.
SMART; SM00408; IGC2; 2.
SMART; SM00408; IGC2; 2.
Receptor; Immunoglobulin domain; G.
Repeat; Blood group antigen.
SIGNAL
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SEQUENCE OF 1-588 FROM N.A.

MEDILINE-9504297; PubMed-7954395;

Campbell I.G., Foulkes W.D., Senger G., Trowsdale J.,

Garin-Chesa P., Rettig W.J.;

"Molecular cloning of the B-CAM cell surface glycoprotein of

"Molecular cloning of the B-CAM cell surface glycoprotein of

epithelial cancers: a novel member of the immunoglobulin

superfamily.";

Cancer Res. 54:5761-5765(1994).

-i- FUNCTION: PROBABLE RECEPTOR. MAY MEDIATE INTRABLLULAR SIGNALING.

-i- FUNCTION: PROBABLE RECEPTOR. MAY MEDIATE PROTEIN.

-i- FUNCTION: PROBABLE RECEPTOR.

-i- TISSUE SPECIFICITY: WIDE TISSUE DISTRIBUTION (HIGHEST IN THE

PANCREAS AND VERY LOW IN BRAIN). CLOSELY ASSOCIATED WITH THE BAS

LAYER OF CELLS IN EPITHELIA AND THE ENDOTHELIUM OF BLOOD VESSEL

LAYER OF CELLS IN EPITHELIA AND THE ENDOTHELIUM OF BLOOD VESSEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lutheran blood group glycoprotein precursor (B-CAM cell
glycoprotein) (Auberger B antigen) (FB/G253 antigen).
LU OR BCAM OR MSK19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X83425; CAA58449.1; -. EMBL; X80026; CAA56327.1; -. Genew; HGNC:6722; LU.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Fibroblast growth factor receptor 4 precursor
(Protein-tyrosine kinase receptor MPK-11).
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                          Gilardi-Hebenstreit P., Nieto M.A., Frain M., Mat Chestler A., Wilkinson D.G., Charnay P.;
"An Eph-related receptor protein tyrosine kinase expressed in the developing mouse hindbrain.";
Oncogene 7:249-2506(1992).
-i- FUNCTION: PUTATIVE RECEPTOR FOR BASIC FIBROBL MAX BE INVOLVED IN THE DEVELOPMENT OF SKELETA
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                                                                                             STRAIN-C57BL/6; TISSUE-Embryonic brain; MEDLINE-93096484; PubMed-1281307;
                                                                                                                  SEQUENCE OF 620-676 FROM N.A.
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                                                                                                                                                                                                         SEQUENCE FROM
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                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                "FGFR-4, a new member of the fibroblast growth fa family, expressed in the definitive endoderm and lineages of the mouse.";
Development 113:641-651(1991).
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tyrosine phosphate
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CYTOPLASMIC (POTENTIAL).

IG-LIKE V-TYPE DOMAIN 1.

IG-LIKE V-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 3.
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Prodom; PD000001; Euk_pkinase; 1.
SMART; SM00408; IGC2; 3.
SMART; SM00219; TYFKC; 1.
PROSTIE; PS00107; PROTEIN_KINASE_ATP; EAPROSTIE; PS00109; PROTEIN_KINASE_DOM; 1.
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RX MEDLINE-9808757,
RA Yamakawa K., Hu
RA Lyons G.E., Kor,
RT "DSCAM: a novel
    Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.-S., Toyoda A., Ishi K., Totoki Y., Choi D.-K., Soeda E., Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A., Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Aaskawa S., Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E., Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P., Minoshima S., Shimizu N., Nordsiek G., Henrischer K., Brandt P., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H., Ramser J., Beck A., Klayes S., Hennig S., Riesselmann L., Dagand E., Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F., Mehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F., The Park Revised Company C., Park R., Vaspo M.-L.;
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                                                                                     use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
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[3]
                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
                                                                                                                                                                                            I ALTERNATIVE POODCTS: 2 ISOFORMS; A LONG FORM/CHD2-52 (SHOWN AND A SHORT FORM/CHD2-42; ARE PRODUCED BY ALTERNATIVE SPLICI-1-TISSUE SPECIFICITY: PRIMARILY EXPRESSED IN BRAIN.

SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERRAMILY.
SIMILARITY: CONTAINS 10 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
SIMILARITY: CONTAINS 6 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                   "The DNA Sequence of human Chromosome 21.";

Nature 405:311-319 (2000).

-!- FUNCTION: CELL ADHESION MOLECULE THAT CAN MEDIATE CATION-
INDEDENDENT HOMOPHILIC BINDING ACTIVITY. COULD BE INVOLVED
NERVOUS SYSTEM DEVELOPMENT.

-!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (PROBABLE). 1
SHORT ISOFORM MAY BE SECRETED.

SHORT ISOFORM MAY BE SECRETED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "DSCAM: a novel member of the immunoglobulin superfamily bown syndrome region and is involved in the development of nervous system"."
Hum. Mol. Genet. 7:227-237(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agarwala K.L., Nakamura S., Tsutsumi Y., Yamakawa K.;
"Down syndrome cell adhesion molecule DSCAM mediates homophilic intercellular adhesion.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
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Yamakawa K., Huot Y.-K., Haendelt M.A., Hubert R.,
Lyons G.E., Korenberg J.R.;
DSCAM: a novel member of the immunoglobulin superi
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AF023449;
AF217525;
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AL163282;
AL163281;
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 AAC17967.1;
AAC17966.1;
AAF27525.1;
CAB90464.1;
CAB90436.1;
CAB90444.1;
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); IPR003952; FnIII.repeat.

); IPR003056; Ig_MHC.

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CYTOPLASMIC (POTENTIAL).

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IG-LIKE C2-TYPE DOMAIN 6.

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IG-LIKE C2-TYPE DOMAIN 8.

IG-LIKE C2-TYPE DOMAIN 9.

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MISSING (IN SHORT ISOFORM).

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SRTLKRPTYLEPIPMEAASSASSTREGGSWQPGAVAFLPQR
EGAELGQAKWASSQNESLLDSRGHLKGNNPYAKSYTLV ->
IGQVTSYICLHTLEWTPC (IN REF. 1).
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Best Local
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Nephrin precursor (Renal glomerulus-specific
                 EMBL; AF168466; AAF03368.1; MGD; MGI:1859637. NGL-
                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-slb.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Podocin, a raft-associated component of the diaphragm, interacts with CD2AP and nephrin."
J. Clin. Invest. 108:1621-1629(2001).
                                                                                                                                                                                                                                                                                                                                                                              <del>:</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J. Clin. Invest. 108:1621-1629(2001).
-I- FUNCTION: Seems to play a role in the development.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shaw A.S., Holzman L.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shih N.Y., Li J., Cotran R., Mundel P., "CD2AP localizes to the slit diaphragm novel C-terminal domain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION MEDLINE-99436348; PubMed-10504499; Holzman L.B., St John P.L., Kovari I.A., Verabrahamson D.R.;
                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schwarz K., Simons M., Reiser J., S
Shaw A.S., Holzman L.B., Mundel P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INTERACTION WITH CD2AP AND NPHS2. MEDLINE=21590460; PubMed=11733557;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cel
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                              - ! - TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₽.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-21590051; PubMed-11733379;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INTERACTION WITH CD2AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Pathol.
                                                                                                                                                                                                                                               PTM: Phosphorylated on tyrosine residues (By similarity).
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.
SIMILARITY: CONTAINS 8 IMMUNOGLOBULIN-LIKE DOMAINS.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: Type I membrane protein (Po at podocyte slit diaphragm between podocyte foot TISSUE SPECIFICITY: Expressed in kidney glomeruli
                                                                                                                                                                                                                                                                                                                                                                                                                                      the kidney glomerular filtration barrier. May slit diaphragm to the actin cytoskeleton.
                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: Interacts with podocin/NPHS2 and with CD2AP C-terminal
                                                                                                                                                                                                                                                                                                                                                                                                 domain.
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26.3%;
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                                                                                                     (See http://www.isb-sib.ch/announce/
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                  Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                Nephrin precursor
NPHS1 OR NPHN.
                                                                                     09R044; Q9QXX7;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last seq
15-JUN-2002 (Rel. 41, Last ann
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SMART; SM00410; IG_like; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00060; FN3;
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Pfam; PF00047; ig; 8.
SEQUENCE FROM N.A.
                                                       Rattus norvegicus
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IPR003598; Ig_c2.
IPR003600; Ig_like.
IPR000399; TPP_enzyme.
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                                                                                                                                   STANDARD;
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41, Last annotation update)
(Renal glomerulus-specific
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                                Chordata;
Rodentia;
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29.5%;
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IG-LIKE C2-TYPE DOMAIN 1.
IG-LIKE C2-TYPE DOMAIN 2.
IG-LIKE C2-TYPE DOMAIN 3.
IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 5.
IG-LIKE C2-TYPE DOMAIN 6.
IG-LIKE C2-TYPE DOMAIN 7.
IG-LIKE C2-TYPE DOMAIN 7.
IG-LIKE C2-TYPE DOMAIN 7.
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                               Craniata; Ver
Sciurognathi;
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                                          Euteleostomi;
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cytoskeleton.";

and J. Physiol. 282:F585-F591(2002).

I. FUNCTION: Seems to play a role in the development or function of the cytoskeleton.

C the kidney glomerular filtration barrier. May anchor the podocy.

C slit diaphragm to the cytoskeleton.

C -I- SUBGUNIT: Interacts with podocin/NPHS2 and with CD2AP C-terminal domain (By similarity).

C -I- SUBCELLUIAR LOCATION: Type I membrane protein (Potential). Locate prodocyte slit diaphragm between podocyte foot processes.

C -I- ALTERNATIVE PRODUCTS: 3 isoforms; isoform 1 (shown here), 2/all and 3/beta; may be produced by alternative splicing.

C -I- SINSIE SPECIFICITY: Specifically expressed in the podocytes of kidney glomeruli.

C -I- SINILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

-I- SIMILARITY: CONTAINS 8 IMMUNOGLOBULIN SUPERFAMILY.

SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                            EMBL; AF125521; AAF12734.1; ...
EMBL; AF161715; AAF14884.1; ...
InterPro; IPR003961; FN III
InterPro; IPR003906; Ig_MHC.
InterPro; IPR003598; Ig_C2.
InterPro; IPR003598; Ig_C2.
InterPro; IPR003599; Ig_Like.
Pfam; PF00041; fn3; 1.
Pfam; PF00047; 1g; 8.
SMART; SM00408; IG_21; 1.
SMART; SM00408; IG_21; 1.
SMART; SM00408; IG_21; 1.
SMART; SM00408; IG_11ke; 6.
Ceall adhesion; Transmembrane; Si.
CHAIN
CHAIN
TRANSMEM
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DOMAIN
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                                                                                                                                                                                                                                                                                              Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21868269; PubMed-11880318;
Yuan H., Takeuchi E., Salant D.J.;
"Podocyte slit-diaphragm protein nephrin
cytoskeleton.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteinuric states.";
Kidney Int. 57:1949-1961(2000).
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domain; Repeat
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ne: Signal; Glycoprotein;
sat; Phosphorylation; Alternative si
portential.

NEPHRIN.

EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 3.

IG-LIKE C2-TYPE DOMAIN 3.

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the podocyte
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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SEQUENCE FROM N.A.

TISSUE=Mammary gland;
MEDLINE=931948A7; pubMed=7680645;
Men D., Reich R., Chedid M., Lengel C., Cc
Neufeld G., Miki T., Tronick S.R.;
"Fibroblast growth factor receptor 4 is a
both acidic and basic fibroblast growth factor.";
J. Biol. Chem. 268:5388-5394(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

MEDLINE=91224085; PubMed-1709094;

Partanen J.M., Maekelae T.P., Eerola E., Korhonen J., Hirvonen Claesson-Welsh L., Alitalo K.;

"RGFR-4, a novel acidic fibroblast growth factor receptor with distinct expression pattern.";

EMBO J. 10:1347-1354(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PGR4_HUMAN STANDARD; PRT; 802 AA. P22455; Q14309; O43785; O1-AUG-1991 (Rel. 19, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Fibroblast growth factor receptor 4 precursor FGFR4 OR JTK2 OR TKF.
SEQUENCE FROM N.A.
MEDLINE=98119018; PubMed=9457674;
Kostrzewa M., Muller U.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LGV-NVTSTEVYGAFTCSIQNISFSSFT
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Catarrhini;
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i; Hominidae; Homo.
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Pfam; PR00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1
SNART; SM00409; IG; 3:
SNART; SM00410; IG_like; 2.
SNART; SM00408; IGC2; 3.
SNART; SM00220; S.TKC; 1.
SMART; SM002219; TYrKC; 1.
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                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR003006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: RECEPTOR FOR ACIDIC FIBROBLAST GROWTH FACTOR. DOES BIND TO BASIC FIBROBLAST GROWTH FACTOR. BINDS FGF19.

CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
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                                                                                                                                                                                                                                                                                                                         Signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003598; Ig_c2.
IPR003600; Ig_like.
IPR002290; Ser_thr_pkinase.
IPR001245; Tyr_pkinase.
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O THE
                                                                                                                         CYTOPLASMIC (POTENTIAL).
IG-LIKE C2-TYPE DOMAIN 1
IG-LIKE C2-TYPE DOMAIN 2
IG-LIKE C2-TYPE DOMAIN 3
IG-LIKE C2-TYPE DOMAIN 3
PROTEIN KINASE.
ATP (BY SIMILARITY).
ATP (BY SIMILARITY).
POTENTIAL.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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FIBROBLAST GROWTH FACTOR RECEPTOR
EXTRACELULAR (POTENTIAL).
                                                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                                                                                                                                                                                                          Transmembrane;
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FIBROBLAST
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GROWTH F
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Pfam; PF00041; fn3; Pfam; PF00047; ig; PRINTS; PR00014; FN

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FN3; FNTYPEIII InterPro;
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; IPR003961; FN_III.
; IPR003962; FnIII_repeat.
; IPR003065; Ig_MIC.
; IPR003606; Ig_Like.
; IPR003600; Ig_like.

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15-JUL-1999 (Rel. 38, Last sequence update)
15-JUR-2002 (Rel. 41, Last annotation update)
Myosin-binding protein C, fast-type (Fast MyBP-C) (C-protein, skeletal
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Mammalia; Eutheria; Primates;
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Matches 27
SUBCELLULAR LOCATION.

MEDLINE-9934171; PubMed-10393930;

RUOTSALAINEN V. LJUNGBORG P., Wart.

Kestilae M., Jalanko H., Holmberg C.

"Nephrin is specifically located at

podocytes.";

Proc. Natl. Acad. Sci. U.S.A. 96:790

[5]
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15-JUN-2002 (Rel. 4
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Thick filament; 1
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                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. (ISOFORM 1).
Grunkemeyer J.A., Kumar N., Kalluri R.;
"Human nephrin (NPHS1) cDNA sequence.";
submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. (ISOFORM 1).

MEDLINE=98325371; Pubmed=9660941;

Kestilae M., Lenkkeri U., Maennikkoe M., Lamerdin J., McCready P.

Futaala H., Ruotsalainen V., Morita T., Nissinen M., Herva R.,

Kashtan C.E., Peltonen L., Holmberg C., Olsen A., Tryggvason K.;

"Positionally cloned gene for a novel glomerular protein -- neph
is mutated in congenital nephrotic syndrome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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(Renal glomerulus-specific cell adhesion receptor).
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IG-LIKE C2-TYPE DOMAIN 4.
IG-LIKE C2-TYPE DOMAIN 5.
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                              96:7962-7967(1999)
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            Cell adhesion;
Immunoglobulin
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            domain;
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R InterPro: IPR003961; FN_III
R InterPro: IPR003065; Ig_MHC.
InterPro: IPR003508; Ig_C2.
InterPro: IPR003508; Ig_like
Pfam; PP00041; fn3; 1
Pfam; PP00041; fn3; 1.
SMART; SM00060; FN3; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00408; IGC2; 1.
SMART; SM00408; IGC1; IGC1; IGC2; I.
SMART; SM00408; IGC1; IGC1; IGC2; I.
SMART; SM00408; IGC1; IGC1; IGC2; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Kidney Int. 57:401-404(2000)

-i- FUNCTION: Seems to play a role in the development or function of the kidney glomerular filtration barrier. May anchor the podocyte slit diaphragm to the actin cytoskeleton.

-i- SUBUNIT: Interacts with podocin/NPHS2. Interacts with CD2AP C-

terminal domain (By similarity)

-i- SUBCELLULAR LOCATION: Type I membrane protein (Potential).

Peredominantly located at podocyte slit diaphragm between podocyte foot processes. Also associated with podocyte apical plasma
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MEDLINE-99115081; PubMed-9915943;
Lenkkeri U., Maennikkoe M., McCready P., Lamerdin J., Gribouval O., Miaudet P.M., Antignac C.K., Kashtan C.E., Homberg C., Olsen A., Kestilae M., Trygyavason K.; "Structure of the gene for congenital nephrotic syndrome of the finnish type (NPHS1) and characterization of mutations."; Am. J. Hum. Genet. 64:51-61(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF035835; AAC39687.1;
EMBL; AF190637; AAG17141.1;
EMBL; AF126957; AAA736451.1;
Genew; HGNC:7908; NPHS1.
MIM; 602716; ".
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MEDLINE-20117947; PubMed-10652016;
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MBDLINE=21551283; PubMed=11562357;
Huber T.B., Kottgen M., Schilling B.,
"Interaction with podocin facilitates
J. Biol. Chem. 276:41543-41546(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      glomeruli.

DEVELOPMENTAL STAGE: In 23-week-old embryo found in epithelial podocytes of the periphery of mature and developing glomeruli.

PTM: Phosphorylated on tyrosine residues.

DISEASE: Defects in NPHS1 are the cause of congenital nephrotic syndrome of the finnish type (NPHS1 or CNF); an autosomal recessive disorder characterized by massive proteinuria in utero
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          membrane.

ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2/alpha; are produced by alternative splicing.

TISSUE SPECIFICITY: Specifically expressed in podocytes of kidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and nephrosis at birth.
SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMASIMILARITY: CONTAINS 8 IMMUNOGLOBULIN-LIKE DOMAINS.
Transmembrane; Signal; Glycoprotein; domain; Repeat; Phosphorylation; Alt
                                                                                                                                                                                                                                                                    FN_III.
Ig_MHC.
Ig_c2.
Ig_like.
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signaling.";
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Alternative splicing;

Gaps

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p22437;
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01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Prostaglandin G/H synthase 1 precursor (EC 1.14.99.1) (Cyclooxygenase
-1) (COX-1) (Prostaglandin endoperoxide synthase 1) (Prostaglandin H2
synthase 1) (PGH synthase 1) (PGHS-1) (PHS 1).

PTGS1 OR COX1 OR COX-1.
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                                          between
the Eurc
                                                                                                                                                                                          "The aspirin and heme-binding sites of ovine and murine endoperoxide synthases.";
J. Biol. Chem. 265:5192-5198(1990).
-i- FUNCTION: MAY PLAY AN IMPORTANT ROLE IN REGULATING CELL PROLIFERATION IN SOME NORMAL AND NEOPLASTICALL
                                                             This
                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
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                        use by non-profit institutions as long modified and this statement is not removed
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                                                                         PEROXIDASE.

MISCELLANDOUS: THIS ENZYME IS THE TARGET OF NONSTEROIDAL ANTI-INFLAMMATORY DRUGS SUCH AS ASPIRIN.

SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.

SIMILARITY: BELONGS TO THE PROSTAGLANDIN G/H SYNTHASE FAMILY.
                               s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                      SUBCELLULAR LOCATION: Membrane-associated.
MISCELLANEOUS: THIS ENZYME ACTS BOTH AS A
                                                                                                                                                 H2 + A + H(2)O.
PATHWAY: FIRST
THROMBOXANES.
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H2 + A + H(2)O.
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        equires a license agreement (Semail to license@isb-sib.ch).
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arith E.A., Kraemer
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/FTId=VAR_013052.
R -> C (IN CNF).
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R -> P (IN CNF).
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A -> D (IN CNF).
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               (See http://www.isb-sib.ch/announce/
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Mammalia; Eutheria; P
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EGF-like domai
SIGNAL
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P11362; P17049;

01-JUL-1989 (Rel. 11, Created)

11-JUL-1991 (Rel. 18, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

Basic fibroblast growth factor receptor 1 precursor (EC 2.7.1.112)

(FGFR-1) (bFGF-R) (Fms-like tyrosine kinase-2) (c-fgr).

FGFR1 OR FLG OR FGFBR OR FLT2.
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SMART;
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InterPro; IPR002007; Anim_pero
InterPro; IPR000561; EGF-11ke.
Pfam; PF00008; EGF; 1.
Pfam; PF03098; An_peroxidase;
PRINTS; PR00457; ANPEROXIDASE.
                                  "Isacchi A., Bergonzoni L., Sarmientos P
"Complete sequence of a human receptor
fibroblast growth factors.";
Nucleic Acids Res. 18:1906-1906(1990).
                                                                                           MEDLINE=90245600; PubMed=2159626;
Isacchi A., Bergonzoni L., Sarmientos P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
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PROSITE; PS01186; EGF_2; FALSE_NEG.
Oxidoreductase; Dioxygenase; Peroxidase;
Prostaglandin biosynthesis; Heme; Iron;
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SEQUENCE FROM N.A.
                                                                                                                                  SEQUENCE FROM N.A.
TISSUE⇒Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142
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SM00181; EGF;
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34; Conservative
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Primates;
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CYCLOOXYGENASE (BY SIMILARIA
PROXIMAL HEME LIGAND (BY SI
ASPIRIN-ACETYLATED SERINE.
BY SIMILARITY.
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Pred. No.
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EGF-LIKE.
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Catarrhini;
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Signal; Membrane;
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SEQUENCE FROM ... TISSUE-Placenta; PubMed=2162671; MEDLINE-90290512; PubMed=2162671; Itoh N., Terachi T., Ohta M., Seo M.K.; The complete amino acid sequence of the shorter form The complete amino acid sequence of deduced from its cDt Commun. 169:680-685(1990).
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Robbins K.C.;
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Hou J., Kan M., McKeehan K., McBride
"Fibroblast growth factor receptors f
structural domains.";
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Barton D.E., Francke U., Schlessinger J., Givol D.;
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Hattori Y., Odagiri H., Sugimura T., Terada

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=92118399; PubMed=1662973;
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                                                                                                           MEDLINE=91319400; PubMed=1650441;
                                                                                                                                         SEQUENCE FROM
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              SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                              Mol. Cell. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                        3:9-15(1988).
                                                                                                                                        Ν.Α.,
 Sandstroem
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                                                                                                                                        AND ALTERNATIVE
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l monocytes.";
 Claesson-Welsh
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from
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liver
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L.;
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different isoforms
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M.;
growth factor receptor
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vary in three
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=95179173; PubMed=7874169;
Muenke M., Schell U., Hehr A., Robin N.H., Losken H.W., Schinzel A.,
Pulleyn L.J., Rutland P., Reardon W., Malcolm S., Winter R.M.;
"A common mutation in the fibroblast growth factor receptor 1 gene i
"A common mutation in the fibroblast growth factor receptor 1 gene i
"Pfeifer syndrome.";
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"Structure of the FGF receptor tyrosine kinase domain reveals a novel autoinhibitory mechanism.";
Cell 86:577-587(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nature 358:681-684(1992).
[14]
X-RAY CRYSTALLOGRAPHY (2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jaye M., Schlessinger J.;
"Point mutation in FGF receptor eliminates phosphatidylinositol hydrolysis without affecting mitogenesis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature
[13]
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Peters K.G., Marie J., Wilson E., Ives H.E., Escobedo J.,
del Rosario M., Mirda D., Williams L.T.;
"Point mutation of an FGF receptor abolishes phosphatidylinositol
                                                                  or send
                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor in complex with inhibitors Science 276:955-960(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      x-ray Crystallography (2.4 angstroms) OF MEDLINE-97284786; PubMed-9139660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hubbard S.R., Schlessinger J.;
"Structures of the tyrosine kinase domain
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                                                                                                                                                                                                                                                                                                                                                          TYPOSINE PHOSPHATE.

SUBCELLULAR LOCATION: Type I membrane protein.

ALTERNATIVE PRODUCTS: MANY FORMS OF FGFR1 ARE PRODUCED BY
ALTERNATIVE SPLICING. THE FORM SHOWN HERE IS KNOWN AS ALPHA-A1.

DISEASE: DEFECTS IN FGFR1 ARE ONE OF THE CAUSES OF PFEIFFER
SYNDROME (FS) (ALSO KNOWN AS ACROCEPHALOSYNDACTYLY TYPE V; ACS5);
CHARACTERIZED BY CRANIOSYNOSTOSIS (PREMATURE FUSION OF THE SKULL
SUTURES) WITH DEVIATION AND ENLARGEMENT OF THE THUMBS AND GREAT
TOES, BRACHYMESOPHALANGY, WITH PHALANGEAL ANKYLOSIS AND A VARYING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATALYTIC ACTIVITY: ATP + a protein
                                                                                                                                                                                                                                                                           DISEASE: Involved in a t(8;13)(p12;q12) chromosomal translocation which involves FGFRI AND ZNF198. The resulting transcript is a possible candidate for stem cell leukemia lymphoma syndrome/SCLL. SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWTH FACTOR.
                                                                                                                                                                                                        DATABASE: NAME-Atlas Genet. Cytogenet. Oncol. Haematol.; WWW-"http://www.infobiogen.fr/services/chromcancer/Genes/FGFR1113.html"
                                                                                                                                                                                                                                              SIMILARITY:
                                                                                                                                                                                                                                                                FAMILY
                                                                                                                                                                                                                                                                                                                                                 DEGREE OF SOFT TISSUE SYNDACTYLY.
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                                  x51803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           358:678-681(1992).
                                                                  an email to license@isb-sib.ch).
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CAA36101.1;
CAA37015.1;
CAA47375.1;
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Best Local
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P16092; Q01736; Q61562;
01-APR-1990 (Rel. 14, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Basic fibroblast growth factor receptor 1 precursor (EC 2.7.1.112)
(FGFR-1) (bFGF-R) (MFR).
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STRAIN-BALB/c; TISSUE-Brain; MEDLINE-90265603; PubMed-2161096; Safran A., Avivi A., Orr-Urterege
                                                                                              MEDLINE-90160373; PubMed-1689490; Reid H.H., Wilks A.F., Bernard O.; "Two forms of the basic fibroblast are expressed in the developing mouproc. Natl. Acad. Sci. U.S.A. 87:15
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR00109; TYRKINASE.
ProDom; PD000001; Euk_pkinase;
SMART; SM00408; IGC2; 3.
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                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
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                                                           SEQUENCE FROM N.A
                                                                                                                                                                                               TISSUE-Brain;
                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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PF00069; pkinas
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X57118;
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M37722;
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IPR003598; Ig_c2.
IPR001245; Tyr_pkinase
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CAA40401.1;
CAA40402.1;
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CAA40404.1;
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AAA75007.1;
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Rodentia;
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                                                                                              sic fibroblast growth factor receptor-like mRNA
developing mouse brain.";
i. U.S.A. 87:1596-1600(1990).
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Pred. No. 5.8;
9; Mismatches
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EMBL; M28998: AAA37290.1; -.
EMBL; M5053; AAA37620.1; -.
EMBL; M65053; AAA37622.1; -.
EMBL; M33760; AAA37622.1; -.
EMBL; M33760; AAA37622.1; -.
EMBL; M3760; AAA37622.1; -
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[5]
SEQUENCE OF 1-15 FROM N.A., AND ALTERNATIVE SPLICING.
MEDLINE-95100926; PubMed-7802632;
Harada T., Saito H., Kouhara H., Kurebayashi S., Kasayama
Terakawa N., Kishimoto T., Sato B.;
"Murine fibroblast growth factor receptor 1 gene generates
"Murine fibroblast growth factor receptor 1 alte
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MEDLINE-91207411; PubMed-1708247;
KOUHATA H., KASAYAMA S., Saito H., Matsumoto K., Sato B.;
"Expression cDNA cloning of fibroblast growth factor (FGF) receptor in mouse breast cancer cells: a variant form in FGF-responsive transformed cells.";
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"The mu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extrement the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
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MEDLINE=90272715; PubMed=2161540;
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SIMILARITY: BELONGS TO THE FIBROBLAST GROWTH FACTOR RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine phosphate.
SUBCELLULAR LOCATION: Type I membrane protein.
ALTERNATIVE PRODUCTS: 3 ISOFORMS; A LONG FORM
VARIANT FORM AND A SHORT FORM ARE PRODUCED BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHEM. Biophys. Res. Commun. 205:1057-1063(1994).
FUNCTION: RECEPTOR FOR BASIC FIBROBLAST GROWN FOR ACTOR. A SHORTER FORM OF THE RECEPTOR COULD BE A RECEPTOR FOR ACIDIC FGF (AFGF).
CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
Repeat; Arcc. pOTENTIAL.
                                                      Alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       generates multiple
via alternative
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Q24372;
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15-JUL-1998 (Rel. 36
15-JUN-2002 (Rel. 41
Lachesin precursor.
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Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
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SEQUENCE FROM N.A.
MEDLINE=94038693; PubMed=8223276;
MEDLINE=94038693; PubMed=8223276;
Karlstrom R.O., Wilder L.P., Bastlani M.J.;
Tlachesin: an immunoglobulin superfamily protein whose correlates with neurogenesis in grasshopper embryos.";
Development 118:509-522(1993),
Development 118:509-522(1993),
Development 118:509-522(1993),
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91980 MW;
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(Rel. 36, Last seq
(Rel. 41, Last ann
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N-LINKED (GLCNAC. .) (POTENTIAL).
N-SSING (IN SHORT ISOFORM).
T-> G (IN SHORT ISOFORM).
T-> S (IN REF. 4).
ILO -> HPS (IN REF. 1 AND 3).
G -> A (IN REF. 3).
G -> A (IN REF. 3).
G -> A (IN REF. 3).
I -> M (IN REF. 4).
R -> H (IN REF. 4).
R -> H (IN REF. 4).
R -> D (IN REF. 4).
R -> D (IN REF. 4).
D5A4695FA680926B CRC64;
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annotation update)
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CYTOPLASMIC (POTENTIAL).

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

IG-LIKE C2-TYPE DOMAIN 3.

PROTEIN KINASE.

ATP (BY SIMILARITY).

ATP (BY SIMILARITY).
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POTENTIAL.
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ATP (BY SIMILA
BY SIMILARITY
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Mismatches
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ROLE IN EARLY NEURONAL DIFFERENTIATION

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Search completed: November 14, 2002, 17:30:20 Job time: 16 secs
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Best Local Similarity
Matches 23; Conserv
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SIGNAL 1
CHAIN 26
PROPEP 337
DOMAIN 150
DOMAIN 240
DISULFID 50
DISULFID 157
DISULFID 157
DISULFID 247
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LIPID
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SMART; SM00410; IG_like; 1.
SMART; SM00408; IGc2; 2.
Immunoglobulin domain; Cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L13255; AAC37184.1; -. HSSP; P56276; 1TLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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InterPro; IPR003598; Ig_c2.
InterPro; IPR003600; Ig_like.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FlyBase; FBgn0010238; Lac.
                                                       279
                                                                                                           230 VPRPRLGQALQYDMDLEC-----HIEAYPPPAIVWTKDDIQLANNQHYSISHFA--- 278
                                                                                                                              19 VLRPALGSSVA----LNCTAWVVSGPHCSL---PSVQWLKDGLPLGIGGHYSLHEYSWVK 71
                                                                                 72 ANLSEVLYSSYLGVNYTSTEVYGAFTCSIQN 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN: SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE V-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY).

DEVELOPMENTAL STAGE: EXPRESSED FROM THE ONSET OF NEUROGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AXON OUTGROWTH. SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor (By
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39998 MW;
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                                                                                                                                                                                12.0%;
25.3%;
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REMOVED IN MATURE FORM (POTENTIAL).

IG-LIKE V-TYPE DOMAIN.

IG-LIKE C2-TYPE DOMAIN 1.

IG-LIKE C2-TYPE DOMAIN 2.

POTENTIAL.

POTENTIAL.

POTENTIAL.
                                                                                                                                                                              Score 75;
Pred. No.
                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
GPI-ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
                                                                                                                                                                                                                         D1F513E2B9D886E6 CRC64;
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2.6;
                                                                                                                                                                   37;
                                                                                                                                                                                            Length 359
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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sp_plant:*
sp_virus:*
sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
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sp_mhc:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Q96rw7 homo sapien	Q96sc3 homo sapien	Q9vn14 drosophila	Q8sww3 drosophila	Q23551 caenorhabdi	Q23550 caenorhabdi	Q96aa2 homo sapien	Q08476 gallus gall	Q8wz42 homo sapien	Q10465 homo sapien	070246 mus musculu	Q9vs29 drosophila	Q9vsg5 drosophila	Q9hcd3 homo sapien	Q9jlz8 mus musculu	Q9h733 homo sapien	Description

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Q925S5	Q9JIX1	Q9ET59	Q62838	Q9YHS0	Q8WZB3	Q10466	001761	Q17362	Q15598	Q8WY19	Q28733	P97685	Q9QVN5	Q98SW3	Q63709	Q961W0	Q9W260	Q8R4B3	Q8R4B5	Q95YM2	Q95YM1	Q9XZB7	Q8TD84	Q8WXU7	Q91Z60	094856	Q96HT1	076518
mus	Q9jix1 mus musculu	Q9et59 mus musculu	Q62838 rattus norv	gin	Q8wzb3 homo sapien			Q17362 caenorhabdi			Q28733 oryctolagus	rattus			Q63709 rattus ratt	Q961w0 drosophila	dros	Q8r4b3 mus musculu	տ		Q95yml procambarus			Q8wxu7 homo sapien	Q91z60 rattus norv	homo		076518 caenorhabdi

ALIGNMENTS

Qy	Db	Qy	Quer Best Matcl	SQ	DR DR	DR	DR	DR	DR	DR	RL	RT	RA	RA	RA	RC	RP	RN	0 x	8	8	SO	DE	DT	DT	DT	AC	ID	RESULT
61 HYSLHEYSWVKANLSEVLYSSVLGVNYTSTEVYGAFTCSJONISFSSFTLQRAGPTSH 118	1 MPGVCDRAPDFLSPSEDQVLRPALGSSVALNCTAMVVSGPHCSLPSVQWLKDGLPLGIGG 60	1 MPGVCDRAPDFLSPSEDQVLRPALGSSVALNCTAMVVSGPHCSLPSVQWLKDGLPLGIGG 60	Query Match 100.0%; Score 626; DB 4; Length 410; Best Local Similarity 100.0%; Pred. No. 6e-60; Indels 0; Gaps 0; Matches 118; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	SEQUENCE 410 AA; 45707 MW; 2A7A663D79567ED6 CRC64;	SMART; SM00410; IG_like; 1. SMART; SM00255; TIR; 1.	PRINTS; PRO1559; DUFFYANTIGEN.	Pfam; PF01582; TIR; 1.	InterPro; IPR000157; TIR_domain.	InterPro; IPR003600; Ig_like.	EMBL; AK025099; BAB15066.1;	Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.	"NEDO human cDNA sequencing project.";	Tanaka T., Nakamura Y., Isogai T., Sugano S.;	Okitani R., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T.,	Kawabata A., Hikiji T., Kobatake N:, Inagaki H., Ikema Y., Okamoto.S.,	TISSUE=COLON;	SEQUENCE FROM N.A.	[1]	NCBI_TaxID=9606;		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens (Human).			(TrEMBLrel. 16,	2001	Q9H733;	Q9H733 PRELIMINARY; PRT; 410 AA.	LT 1

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Best Local
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Q9HCD3;
Q9HCD3;
Q1-MAR-2001 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
01-JUN-2002 (TrEMBLrel. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR003306; Ig_MHC.
InterPro; IPR003306; Ig_MHC.
InterPro; IPR00157; TIR_domain.
InterPro; IPR00157; IIR_domain.
Pfam; PF00047; Ig; 1.
Pfam; PF01582; TIR; 1.
SMART; SM00409; IG; 1.
SMART; SM002055; TIR; 1.
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09JLZ8;
01-OCT-2000
01-OCT-2000
01-JUN-2002
                                                                                                      SEQUENCE FROM N.A.

MEDLINE=20450683; PubMed=10997877;

Nagase T., Kikuno R., Nakayama M., Hirosawa M., Ohara O.;

"Prediction of the coding sequences of unidentified human

XVIII. The complete sequences of 100 new cDNA clones from

code for large proteins in vitro.";

DNA Res. 7:273-281(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Penton-Rol G., Polentarutti N., Muzio M., Mantovani A.;
"TIR8: a novel toll/Interleukin-1 receptor family member.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AF113795; AAF26200.1; -.
                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; NCBI_TaxID=9606;
       InterPro;
                        InterPro;
                                                       InterPro;
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                                                                                                                                                                                                                                                                                                         KIAA1639 protein
KIAA1639.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGIRR OR TIR8
                                                                                                                                                                                                                                                                                                                                                                                                                                            w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 HYSLHEYSWYKANLSEVLYSSYLGVNYTSTEVYGAFTCSIQNISFSSFTLQRAGPTSH 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MPGVCDRAPDFLSPSEDQVLRPALGSSVALNCTAWVVSGPHCSLPSVQWLKDGLPLGIGG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAGVCDMAPNFLSPSEDQALGLALGREVALNCTAWVFSRPQCPQPSVQWLKDGLALGNGS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /interleukin-1 receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HESTHEDEMVSANESEI-VSSVLVLNLTNAEDYGTETCSVWNVSSHSETLWRAGPAGH 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYSLHEYSWVKANLSEVLVSSVLGVNVTSTEVYGAFTCSIQNISFSSFTLQRAGPTSH 118
                                                                        AB046859; BAE
P56276; ITLK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 67.8
30; Conservative
       IPR000719; Euk_pkinase.
IPR003961; FN_III.
IPR001899; Gram_pos_anc
IPR003599; Ig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel.) (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                       BAB13465.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sigirr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45707 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.1%;
67.8%;
       Gram_pos_anchor
Ig.
                                                                                                                                                                                                                                                                                                                                           16,
16,
21,
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15,
21,
                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8;
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                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 407.5; DB 11;
Pred. No. 4.1e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence up
                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DC4AB99A72356A13 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                               1319
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on update)
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                                                                                                                                         genes.
brain which
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     Дb
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DR PRODOM; PD000001; ENK_PKinase; 2.

DR SMART; SM00060; EN3; 1.

SMART; SM00409; IG; 1.

SMART; SM00409; IG; 1.

R SMART; SM00409; IG; 1.

R SMART; SM00220; S_TKG; 1.

R SMART; SM00220; S_TKG; 1.

R PROSITE; PS00343; GRAM_POS_ANCHORING; UNKNOWN_1.

R PROSITE; PS50011; PROTEIN_KINASE_DOM; 2.
RX MEDILINE-20196006; PubMed=10731132;
RX Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Champe M., Feiffer B.D.,
RA Barndon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barndon R.C., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Gerry J.M., Cawley S., Dahlke C., Daveport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Daveport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Daveport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Daveport L.B., Dew I., Dietz S.M.,
RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Godson K., Doup L.E., Downes M., Dugan-Rocha S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Havey D., Heiman T.J., Wei M., H., Ibegyam C.,
RA Kimmel B.E., Kodira C.D., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            O9VSG5 PRELIMINARY;
O9VSG5;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003598; Ig_C2.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003290; Ser_thr_pkinase.
InterPro; IPR001245; Tyr_pkinase.
Pfam; PF00047; ig_l.
Pfam; PF00069; pkinase; 2.
Prans, PF00069; pkinase; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CG18630 protein.
CG18630.
                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN=BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunoglobulin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               813
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 DRAPDFLSPSEDQVLRPALGSSVALNCTAWVVSGPHCSLPSVQ--WLKDGLPLGIGGHYS 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----ESSSRVLISATLKNFQLLTILVVVAEDLGVYTCSVSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DRAPTFLRELSDETV--VLGQSVTLACQV-----SAQPAAQATWSKDGAPL-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11; Mismatches
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Last sequence update)
Last annotation update)
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FBA43AE17204EF48 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              534
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weison D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Parleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhau K., Zhu S., Zhao Q., Zheng I.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng S.H., Wgers E.W., Rubin G.M., Venter T.C.;
"The genome sequence of Drosophila melanogaster.";
EMBL, AE003556; AAF50456.1;
DR EMBL, AE003556; RAF50456.1;
Triterro; IPR003598; Id ~?
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Adams M.D. Celniker S.E. Holt R.A. Evans C.A. Gocayne J.D.,
RA Adams M.D. Celniker S.E. Li P.W. Hoskins R.A. Galle R.F.
RA Amanatides P.G., Scherer S.E. Li P.W. Hoskins R.A. Galle R.F.
RA George R.A. Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
RA Sutton G.G. Wortman J.R. Yandell M.D. Zhang Q. Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Boxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Bayayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Charry J.M., Cawley S., Dahlke C., Davenport L.B., Devies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Doldek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart M.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro: IPR003006; Ig_N
Pfam; PF00047; ig; 6.
SMART; SM00408; IGC2; 4.
                                                                                                                                                                                                                                                                                                                                                      STRAIN-BERKELEY;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephygroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CG8618 protein. CG8618.
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                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DASPELLYWESEQTLQP--GPTVSLKCVA--TGNP---LPQFTWSLDGFPIPDSSRFLVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity 29.6
29; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
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29.6%;
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Pred. No. 0.055;
17; Mismatches ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Length 534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
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RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Lidang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McIshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong M., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
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Best Local
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Jalali M.
                                                                                                                                                                                                                                  runc, a novel mouse gene of the expressed predominantly in the de Mech. Dev. 71:201-204(1998).
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01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Putative neuronal cell adhesion molecule (PUNC) (Putative neuronal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003560; AAF50601.1; -. FlyBase; FBgn0035748; CG8618. InterPro; IPR003598; Ig_c2. InterPro; IPR003000; Ig_MHC.
                                                                                                                 MEDLINE=99122837;
Salbaum J.M.;
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-SWISS WEBSTER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cell adhesion molecule,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 070246;
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SMART; SM00408; IGc2; 2.
                                                                                                                                                                        STRAIN-FVB;
                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                        Salbaum J.M.;
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE~98175891;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                 'Genomic structure
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MPGVCDRAPDFLSPSEDQVLRPALGSSVALNCTAWVVSGPHCSLP-SVQWLKDGLPLGIG
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  Genome 10:107-111(1999). AF026465; AAD12133.1; -.
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                                                                                                                                                                                               599-715 FROM N.A
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AA; 32290 MW;
                                                                                                                                           PubMed=9922388
                                                                                                                                                                                                                                                                                                                                                                  PubMed=9507132
                                                                                    and
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                                                                                    chromosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      short form).
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Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Musi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                              developing
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                                                                                                                                                                                                                                                                                                           immunoglobulin superfamily,
                                                                                    localization
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .038;
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                                                                                    of
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Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15;
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RESULT 7

[1] Q10465
[2] PRELIMINARY; PRT; 7962 AA.

AC Q10465;
[3] Q10465;
[4] Q10465;
[5] Q10465;
[6] Q10465;
[7] Q1 PREMELTEL. 01, Created)
[7] Q1 PROM 1996 (TIEMBLITEL. 01, Last sequence update)
[7] Q1 PROM 1996 (TIEMBLITEL. 21, Last annotation update)
[8] Q1 PROM 1996 (TIEMBLITEL. 21, Last annotation update)
[9] Q1 PROM 1996 (TIEMBLITEL. 21, Last annotation update)
[9] Q2 PROM 1996 (TIEMBLITEL. 21, Last annotation update)
[9] Q3 PROM 1996 (TIEMBLITEL. 21, Last annotation update)
[9] Q4 PROM 2996 (TIEMBLITEL. 21, Last annotation update)
[9] Q5 PROM 2996 (TIEMBLITEL. 21, Last annotation update)
[9] Q6 PROM 2996 (TIEMBLITEL. 21, Last annotation update)
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                                                                                                   CC -!- TISSUE SPECIFICITY: MUSCLE-SPECIFIC.
CC -!- TISSUE SPECIFICITY: MUSCLE-SPECIFIC.
CC -!- SIMILARITY: TO THE CATALYTIC DOMAINS OF OTHER SERINE/THREONINE
CC -!- SIMILARITY: BELONGS TO IMMUNOGLOBULIN SUPERFAMILY. CONTAINS 90
CC IMMUNOGLOBULIN C2-FIKE DOMAINS.
CC EMBL; X90569: CAA62189.1; --
DR HSSP; P56276; ITLK.
DR HSSP; P56276; ITLK.
DR InterPro; IPRO03508; Ig_-Ike.
DR InterPro; IPRO03508; Ig_-MHC.
DR InterPro; IPRO03608; Ig_-MHC.
DR InterPro; IPRO03108; PPAK_motif.
DR InterPro; IPRO04168; PPAK_motif.
DR Pfam; PF00047; Iq; 59.
DR SMART; SM004408; IGc2; 43.
DR SMART; SM00440; IG_Ike; 15.
DR SMART; SM00440; IG_Ike; 15.
SMART; SM00410; IG_IRE; Alternative splicing; Repeat; KM
M Serine/threonine-protein kinase; Alternative splicing; Repeat;
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HSSP; P80362; IWTL.
MGD; MGI:1202390; Punc.
InterPro; IPR003961; FN_II
InterPro; IPR003961; IG_C2
InterPro; IPR003006; IG_MEDIAN FN_II
INTERPRO; IPR003006; IG_MEDIAN FN_II
Pfam; PF00041; fn_3; 2.
Pfam; PF00047; ig; 4.
SMARF; SM00408; IGC2; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Titins: giant proteins in charge of muscle ultrastructure and elasticity.";
Science 270:293-296(1995).
Science 270:293-296(1995) THIS GIANT MUSCLE PROTEIN MAY BE INVOLVED IN MUSCLE PROTEIN THE STRUCTURAL INTEGRITY OF SARCOMERES, MAY HAVE PROTEIN KINASE ACTIVITY.

-I- ALTERNATIVE PRODUCTS: A NUMBER OF FORMS OF THIS PROTEIN ARE PRODUCED BY ALTERNATIVE SPLICING WHICH DIFFER IN TISSUE DISTRIBUTION. DIFFERENT SIZE TRANSCRIPTS MAY ALSO EXIST WITHII ONE TYPESTEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Immunoglobulin doma SEQUENCE 793 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 YSWVKANLSEVLVSSVLGVNVTSTEVYGAFTCSIQNISFSS 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----KNN-----NSTLSISGVGPEDEAIYQCVAENIAGSS
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31; Conser
                                              5618
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                                      GLU/LYS/PRO/VAL-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 94; DB
Pred. No. 0.19
1; Mismatches
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pfam; pF00041; fn3; 132-f
pfam; pF00047; ig; 146.
pfam; pF00047; ig; 146.
pfam; pF00069; pkinase; 1.
pfam; pF002818; ppak; 53.
pr0000m; pF0000001; Euk pkinase;
SMART; SM00060; FN3; 133.
SMART; SM00409; IG; 167.
SMART; SM00409; IG; 118.
SMART; SM00406; IGC; 118.
SMART; SM00406; IGC; 23.
SMART; SM00219; TYrKC; 1.
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McNabb M. Witt C.C., Labeit D., Greg
Labeit S.;
"The complete gene sequence of titin,
kDa titin isoform and its interaction
cline to I-band linking system.";
Circ. Res. 89:1065-1072(2001).
CIRC. RS. 89:1065-1072(2001).
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Q8WZ42;
01-MAR-2002
01-MAR-2002
01-JUN-2002
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Bang M.L., Centher T., Fornoff F., Geach A.J., (
Bang M.L., Witt C.C., Labeit D., Gregorio C.C.,
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MEDLINE=20309627; PubMed=10850961;

Freiburg A., Trombitas K., Hell W., Cazorla O., Fougerousse F.,

Centner T., Kolnerer B., Witt C., Beckmann J.S., Gregorio C.C.,

Granzler H., Labeit S.;

"Series of exon-skipping events in the elastic spring region of

as the structural basis for myofibrillar elastic diversity.";

Circ. Res. 86:1114-1121(2000).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NON_TER
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A; 883018 MW;
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; PPAK_motif.
; Ser_thr_pkinase.
; Tyr_pkinase.
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Euk_pkinase.
FGGY_kin.
FN_III.
HLH_basic.
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Ig_MHC.
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7; Mismatches 32;
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SMART; SM00410; IG_like; 2.
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Pfam; PF00047; ig; 11.
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TISSUE-SKELETAL MUSCLE;
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InterPro; IPR003006; Ig_MHC
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38; Conserv
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PS00038;
PS00290;
PS00435;
PS50011;
PS00109;
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 (TrEMBLrel. (TrEMBLrel.
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0; IG_MGC; UNKNOWN_1.
5; PEROXIDASE_1; UNKNOWN_1.
1; PROTEIN_KINASE_DOM; 1.
9; PROTEIN_KINASE_TYR; UNKNOWN_1.
0 AA; 3816262 MW; 5B1120058A7CE58
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Neognathae; Galliformes; Phasianidae; Phasianinae;
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24.5%;
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Pred. No. 0.51
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7; Mismatches
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Pred. No. 17
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Best Local
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Q23550; Q27232;
01-NOV-1996 (TIEMBLIFE). 01
01-NOV-1998 (TIEMBLIFE). 08
01-MAR-2002 (TIEMBLIFE). 20
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Pfam; PF00047; 19; 49.
Pfam; PF00612; IO; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00621; RhoGEF;
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Submitted
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PROSITE;
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InterPro;
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MEDLLINE=90044042; PubMed=2812002;
Benian G.M., Kiff J.E., Neckelmann N., N
"Sequence of an unusually large protein
myosin activity in C. elegans.";
Nature 342:45-50(1989).
                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                          UNC-22 protein.
UNC-22 OR ZK617.1.
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 STRAIN-BRISTOL
                   SEQUENCE OF 784-6831
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27; Conserv
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IPR000219; RhoGEF.
IPR001412; tRNA-synt_I.
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Pred. No. 5.4;
24; Mismatches
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Catarrhini;
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01-NOV-1998 (TIEMBLE 0
01-MAR-7002 (TIEMBLE 0
01-MAR-7002 (TIEMBLE 0
UNC-22 OR ZK617.1.
                                                                                                                           Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda;
Rhabditidae; Peloderinae; Cae
SEQUENCE FROM N.A.
Harris B., White S.;
Submitted (MAY-1996) to t)
-!- ALTERNATIVE PRODUCTS:
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11. ALTERNATIVE PRODUCTS: TWO FORMS; ISOFORM ZK617.1A (1993).
11. SOFORM ZK617.1B (Q23551); MAY BE PRODUCED BY ALTERNATION CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM CANADAM
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Pred. No. 5.6;
21; Mismatches
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  (Q23550) AND
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SPLICING.

C. SPLICING.

C. I. SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL; 27389; CAA98082.1; JOINED.

REMBL; 273897; CAA98085.1; JOINED.

REMBL; 273897; CAA98065.1; JOINED.

REMBL; 273897; CAA98065.1; JOINED.

REMBL; 273899; CAA980.1; JOINED.

REMBL; 273899; CAA980
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Matches 23
                                                              Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Friee E., George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M., Celniker S.,
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Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

NCBI_TaxID-7227;
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AY095040; AAM11368.1; -.
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                          RA Harris N.L. Harvey D. Heiman T.J., Hernander J.R., Houck J.,
RA Harris N.L. Havey D. Heiman T.J., Hernander J.R., Houck J.,
RA Harris N.L. Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,
RA Merkulov G., Milshina N.V., Wobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shier B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu X., Smith H.O.,
RA Zheng R.A., Wyers E.W., Rubin G.M., Venter J.C.,
RT "The genome sequence of Drosophila melanogaster.";
DR KMRI. ARON3606 ANSO2177 1: -
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Baril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bermann B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Durbin K.J., Evangelista C.C., Ferriera S., Dunkov B.C., Dunn P.,
Durbin K.J., Evangelista C.C., Ferriera S., Fleischmann W.,
Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasset K.,
RA Harris N.I., Harvey D., Heiman T.J., Hernander T.B., Houck T.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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01-MAY-2000 (TrEMBLrel.
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                     AE003606; AAF52137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 88; DB
Pred. No. 0.92
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 5; Length 1036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .92;
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δõ

12 LSPSEDQVLRPALGSSVALNCTAWVVSGPHCSLPSVQWLKDGLPLGIGGHYSLHEYSWVK 71

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Вb
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00059; lectin_c; l.

Pfam; PF00059; lectin_c; l.

SMART; SM000034; CLECT; l.

SMART; SM00060; FN3; 4.

SMART; SM00408; IGC2; 3.

SMART; SM00410; IG_like- ?

PROSTTE
                                                                                Pfam; PF00008; EGF; 5.
Pfam; PF000097; 19; 17.
Pfam; PF000090; tsp 1; 6.
PROSITE; PS00010; ASX_HYDF
PROSITE; PS00266; CECROPIT
PROSITE; PS01186; EGF_CA;
PROSITE; PS01187; EGF_CA;
                                                                                                                                                                                                                                                                                                                                                                                                          Q96SC3
Q96SC3;
01-DEC-2001 (TrembLrel. 1
01-DEC-2001 (TrembLrel. 1
01-JUN-2002 (TrembLrel. 2
                                                                                                                                                                           "Partial sequence of fibulin-6 with a c-terminal region domain II and III of the fibulin family.";

Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ306906; CAC37630.1; -.

InterPro; IPR000152; Asx_hydroxyl.

InterPro; IPR000875; Cecropin.

InterPro; IPR000875; Cecropin.

InterPro; IPR0008161; EGF-Ca.

InterPro; IPR001881; EGF_Ca.

InterPro; IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Homo sapiens (Human).
Theria; Metazoa; Chordata;
Theria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                Fibulin-6 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam;
                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                        Kostka G.,
                                                                                                                                                                                                                                                                                                     TISSUE-MELANOMA;
                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FlyBase; FBgn0037240;
                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLSMKPSFKKHPLESEVY-----AVYNGNTTIVCDPEAAPRPKFQWKKDGQVIGSGGH 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VCDRAPDFLS-PSEDQVLRPALGSSVALNCTAWVVSGPHCS-LPSVQWLKDGLPLGIGGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00041; fn3; PF00047; ig;
  l Similarity 28.6
26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                  PS00268; CECROPIN; UNKNOWN_1.
PS01186; EGF_2; UNKNOWN_3.
PS01187; EGF_CA; UNKNOWN_8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; IPR003598; Ig_c2.
; IPR003600; Ig_like.
; IPR003006; Ig_MHC.
; IPR001304; Lectin_C.
                                                                        PS50092;
                                                                                                                                                                    IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003961;
                                                                                                                                                                                                                                                                                        Timpl R.;
                                                2673 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1336 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG_like; 2.
1; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -RRILPSGTLTISPTSRDDEGIYTCIASN 777
                                                                        TSP1;
                                                                                                                      ASX_HYDROXYL; UNKNOWN_5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ); CG1084.
             14.1%;
28.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.1%;
27.7%;
                                               291017 MW; BEAEC30B8340E272 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151994 MW; 1636094A64484262 CRC64;
  13;
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 88;
Pred. No.
             Score 88;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                  Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            2673
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1.3;
                          DB
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                        4;
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  32;
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                       Length 2673;
  Indels
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  20;
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Gaps
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Search completed: November 14, 2002, 17:31:05 Job time : 42 secs